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<110> Pasteur Mérieux Sérums et Vaccins
INSERM

<120> Nucleic acids and polypeptides specific for the
pathogenic strains of the Neisseria genus

<130> BET 99/0918

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<150> FR 98 13 893

<151> 1998-10-30

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<170> PatentIn Ver. 2.1

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Replase
Patent # 3/A

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003043-0860

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Ser	Ala	Gln	Ala	Glu	Asn	Glu	Met	Ala	Ile	Leu	Asn	Leu	Ile	Gly	Lys				
305					310					315					320				
Lys	Trp	Ile	Asp	His	Leu	Ile	Gln	Pro	Thr	Gln	Leu	Gly	Tyr	Gly	Asn				
			325					330						335					
Gly	Asp	Asn	Met	Pro	Asp	Glu	Lys	Leu	Leu	Pro	Leu	Phe	Asp	Lys	Ile				
			340					345					350						
Asn	Leu	Gln	Gln	Gly	Arg	His	Phe	Ile	Val	Leu	His	Gln	Arg	Gly	Ser				
		355					360					365							
His	Ala	Pro	Tyr	Ser	Ala	Leu	Leu	Gln	Pro	Gln	Asp	Lys	Val	Phe	Gly				
	370					375					380								
Glu	Leu	Ile	Val	Asp	Lys	Tyr	Asp	Asn	Thr	Ile	His	Lys	Thr	Asp	Gln				
385					390				395					400					
Met	Ile	Gln	Thr	Val	Phe	Glu	Gln	Leu	Gln	Lys	Gln	Pro	Asp	Gly	Asn				
			405					410						415					
Trp	Leu	Phe	Ala	Tyr	Thr	Ser	Asp	His	Gly	Gln	Tyr	Val	Arg	Gln	Asp				
			420				425						430						
Ile	Tyr	Asn	Gln	Gly	Thr	Val	Gln	Pro	Asp	Ser	Tyr	Leu	Val	Pro	Leu				
	435						440					445							
Val	Leu	Tyr	Ser	Ser	Asn	Lys	Ala	Val	Gln	Gln	Ala	Ala	Asn	Gln	Ala				
	450					455					460								
Phe	Ala	Pro	Cys	Glu	Ile	Ala	Phe	His	Gln	Gln	Leu	Ser	Thr	Phe	Leu				
465					470					475					480				
Ile	His	Thr	Leu	Gly	Tyr	Asp	Met	Pro	Val	Ser	Gly	Cys	Arg	Glu	Gly				
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Ser	Val	Thr	Gly	Asn	Leu	Ile	Thr	Gly	Asp	Ala	Gly	Ser	Leu	Asn	Ile				
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Arg	Asp	Gly	Lys	Ala	Glu	Tyr	Val	Tyr	Pro	Gln									
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Met	Ala	Leu	Ala	Val	Ala	Thr	Thr	Leu	Ser	Ala	Cys	Leu	Gly	Gly	Gly	
			20					25					30			
ggc	ggc	act	tct	gcg	ccc	gac	ttc	aat	gca	ggc	ggc	acc	ggg	atc	ggc	144
Gly	Gly	Thr	Ser	Ala	Pro	Asp	Phe	Asn	Ala	Gly	Gly	Thr	Gly	Ile	Gly	
		35				40						45				
agc	aac	agc	aga	gca	aca	aca	gcg	aaa	tca	gca	gca	gta	tct	tac	gcc	192
Ser	Asn	Ser	Arg	Ala	Thr	Thr	Ala	Lys	Ser	Ala	Ala	Val	Ser	Tyr	Ala	
	50					55						60				
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Gly	Ile	Lys	Asn	Glu	Met	Cys	Lys	Asp	Arg	Ser	Met	Leu	Cys	Ala	Gly	
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cgg	gat	gac	gtt	gcg	gtt	aca	gac	agg	gat	gcc	aaa	atc	aat	gcc	ccc	288
Arg	Asp	Asp	Val	Ala	Val	Thr	Asp	Arg	Asp	Ala	Lys	Ile	Asn	Ala	Pro	
			85					90						95		
ccc	ccg	aat	ctg	cat	acc	gga	gac	ttt	aca	aac	cca	aat	gac	gca	tac	336
Pro	Pro	Asn	Leu	His	Thr	Gly	Asp	Phe	Thr	Asn	Pro	Asn	Asp	Ala	Tyr	
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Lys	Asn	Leu	Ile	Asn	Leu	Lys	Pro	Ala	Ile	Glu	Ala	Gly	Tyr	Thr	Gly	
		115					120					125				
cgc	ggg	gta	gag	gta	ggg	atc	gtc	gat	aca	ggc	gaa	tcc	gtc	ggc	agc	432
Arg	Gly	Val	Glu	Val	Gly	Ile	Val	Asp	Thr	Gly	Glu	Ser	Val	Gly	Ser	
	130					135					140					
ata	tcc	ttt	ccc	gaa	ctg	tat	ggc	aga	aaa	gaa	cac	ggc	tat	aac	gaa	480
Ile	Ser	Phe	Pro	Glu	Leu	Tyr	Gly	Arg	Lys	Glu	His	Gly	Tyr	Asn	Glu	
145					150					155					160	
aat	tac	aaa	aac	tat	acg	gcg	tat	atg	cgg	aag	gaa	gcg	cct	gaa	gac	528
Asn	Tyr	Lys	Asn	Tyr	Thr	Ala	Tyr	Met	Arg	Lys	Glu	Ala	Pro	Glu	Asp	
			165					170						175		
gga	ggc	ggg	aaa	gac	att	aaa	gct	tct	ttc	gac	gat	gag	gcc	gtt	ata	576
Gly	Gly	Gly	Lys	Asp	Ile	Lys	Ala	Ser	Phe	Asp	Asp	Glu	Ala	Val	Ile	
			180					185					190			
gag	act	gaa	gca	aag	ccg	acg	gat	atc	cgc	cac	gta	aaa	gaa	atc	gga	624
Glu	Thr	Glu	Ala	Lys	Pro	Thr	Asp	Ile	Arg	His	Val	Lys	Glu	Ile	Gly	
		195														

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Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn	
225 230 235 240	
acg cat gat gga acc aag aac gaa ata atg tct gca gcc atc cgc aat	768
Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser Ala Ala Ile Arg Asn	
245 250 255	
gca tgg gtc aag ctg ggc gaa cgt ggc gtg cgc atc gtc aat aac agt	816
Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser	
260 265 270	
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Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp His Phe Gln Ile Ala	
275 280 285	
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Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Ala Tyr Ser Gly Gly	
290 295 300	
gat aaa aca gac gag ggt atc cgc ctg atg caa cag agc gat tac ggc	960
Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly	
305 310 315 320	
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Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser	
325 330 335	
gca agc aat gac gca caa gct cag ccc aac aca ctg acc cta ttg cca	1056
Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr Leu Thr Leu Leu Pro	
340 345 350	
ttt tat gaa aaa gat gct caa aaa ggc att atc aca gtc gca ggc gta	1104
Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val	
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Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn His Cys Gly Ile Thr	
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Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr	
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Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile	
405 410 415	
gta acc ggc acg gcg gct ctg ctg ctg cag aaa tac ccg tgg atg agc	1296
Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser	
420 425 430	
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Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly	
435 440 445	
gca gtc ggc gtg gac agc aag ttc ggc tgg gga ctg ctg gat gcg ggt	1392
Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly	
450 455 460	

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Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala	
465 470 475 480	
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Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile	
485 490 495	
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Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu	
500 505 510	
cac ggc aac aac acc tat acg ggc aaa acc att atc gaa ggc ggt tcg	1584
His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser	
515 520 525	
ctg gtg ttg tac ggc aac aac aaa tcg gat atg cgc gtc gaa acc aaa	1632
Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys	
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Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser	
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gac ggc att gtc tat ctg gca gat acc gac cga tcc ggc gca aac gaa	1728
Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg Ser Gly Ala Asn Glu	
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acc gtg cac atc aaa ggc gat ctg cag ctg ggc ggc gaa ggt acg ctg	1776
Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly Gly Glu Gly Thr Leu	
580 585 590	
tac aca cgt ttg ggc aaa ctg ctg aaa gtg gac ggt acg gcg atg acc	1824
Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Met Thr	
595 600 605	
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Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu	
610 615 620	
aac cgt acc gga caa cgt gtt ccc ttc ctg agt gcc gcc aaa atc ggg	1920
Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly	
625 630 635 640	
cgg gat tat tct ttc ttc aca aac atc gaa acc gac ggt ggt ctg ctg	1968
Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu	
645 650 655	
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Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr	
660 665 670	
ctg tcc tat tat gtc cgt cgc ggc aat gcg gca cgg act gct tcg gca	2064
Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala	
675 680 685	
gcg gca cat tcc gcg ccc gcc ggt ctg aaa cac gcc gta gaa cag gcc	2112
Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly	
690 695 700	

ggc agc aat ctg gaa aac ctg atg gtc gaa ctg gat gcc tcc gaa tca Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser 705 710 715 720	2160
tcc gca aca ccc gag acg gtt gaa act gcg gcc gcc gac cgc aca gat Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp 725 730 735	2208
atg ccg ggc atc cgc ccc tac ggc gca act ttc cgc gca gcg gca gcc Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala 740 745 750	2256
gta cag cat gcg aat gcc gcc gac ggt gta cgc atc ttc aac agt ctc Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu 755 760 765	2304
gcc gct acc gtc tat gcc gac agt acc gcc gcc cat gcc gat atg cag Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln 770 775 780	2352
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ggc ctg cgc gtc atc gcg caa acc caa cag gac ggt gga acg tgg gaa Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu 805 810 815	2448
cag ggc ggt gtt gaa ggc aaa atg cgc ggc agt acc caa acc gtc gcc Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly 820 825 830	2496
att gcc gcg aaa acc gcc gaa aat acg aca gca gcc gcc aca ctg gcc Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly 835 840 845	2544
atg gga cac agc aca tgg agc gaa aac agt gca aat gca aaa acc gac Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp 850 855 860	2592
agc att agt ctg ttt gca ggc ata cgg cac gat gcg ggc gat atc gcc Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly 865 870 875 880	2640
tat ctc aaa ggc ctg ttc tcc tac gga cgc tac aaa aac agc atc agc Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser 885 890 895	2688
cgc agc acc ggt gcg gac gaa cat gcg gaa ggc agc gtc aac gcc acg Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr 900 905 910	2736
ctg atg cag ctg ggc gca ctg ggc ggt gtc aac gtt ccg ttt gcc gca Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala 915 920 925	2784
acg gga gat ttg acg gtc gaa ggc ggt ctg cgc tac gac ctg ctc aaa Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys 930 935 940	2832

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<213> Neisseria meningitidis
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20					25					30									
Gly	Gly	Thr	Ser	Ala	Pro	Asp	Phe	Asn	Ala	Gly	Gly	Thr	Gly	Ile	Gly				
35					40					45									
Ser	Asn	Ser	Arg	Ala	Thr	Thr	Ala	Lys	Ser	Ala	Ala	Val	Ser	Tyr	Ala				
50					55					60									
Gly	Ile	Lys	Asn	Glu	Met	Cys	Lys	Asp	Arg	Ser	Met	Leu	Cys	Ala	Gly				
65					70					75					80				
Arg	Asp	Asp	Val	Ala	Val	Thr	Asp	Arg	Asp	Ala	Lys	Ile	Asn	Ala	Pro				
85					90					95									
Pro	Pro	Asn	Leu	His	Thr	Gly	Asp	Phe	Thr	Asn	Pro	Asn	Asp	Ala	Tyr				
100					105					110									

Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly
 115 120 125
 Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser
 130 135 140
 Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu
 145 150 155 160
 Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp
 165 170 175
 Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile
 180 185 190
 Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly
 195 200 205
 His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly
 210 215 220
 Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn
 225 230 235 240
 Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser Ala Ala Ile Arg Asn
 245 250 255
 Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser
 260 265 270
 Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp His Phe Gln Ile Ala
 275 280 285
 Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Ala Tyr Ser Gly Gly
 290 295 300
 Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly
 305 310 315 320
 Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser
 325 330 335
 Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr Leu Thr Leu Leu Pro
 340 345 350
 Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val
 355 360 365
 Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn His Cys Gly Ile Thr
 370 375 380
 Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr
 385 390 395 400
 Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile
 405 410 415
 Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser
 420 425 430

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Asn	Asp	Asn	Leu	Arg	Thr	Thr	Leu	Leu	Thr	Thr	Ala	Gln	Asp	Ile	Gly	435	440	445
Ala	Val	Gly	Val	Asp	Ser	Lys	Phe	Gly	Trp	Gly	Leu	Leu	Asp	Ala	Gly	450	455	460
Lys	Ala	Met	Asn	Gly	Pro	Ala	Ser	Phe	Pro	Phe	Gly	Asp	Phe	Thr	Ala	465	470	475
Asp	Thr	Lys	Gly	Thr	Ser	Asp	Ile	Ala	Tyr	Ser	Phe	Arg	Asn	Asp	Ile	485	490	495
Ser	Gly	Thr	Gly	Gly	Leu	Ile	Lys	Lys	Gly	Gly	Ser	Gln	Leu	Gln	Leu	500	505	510
His	Gly	Asn	Asn	Thr	Tyr	Thr	Gly	Lys	Thr	Ile	Ile	Glu	Gly	Gly	Ser	515	520	525
Leu	Val	Leu	Tyr	Gly	Asn	Asn	Lys	Ser	Asp	Met	Arg	Val	Glu	Thr	Lys	530	535	540
Gly	Ala	Leu	Ile	Tyr	Asn	Gly	Ala	Ala	Ser	Gly	Gly	Ser	Leu	Asn	Ser	545	550	555
Asp	Gly	Ile	Val	Tyr	Leu	Ala	Asp	Thr	Asp	Arg	Ser	Gly	Ala	Asn	Glu	565	570	575
Thr	Val	His	Ile	Lys	Gly	Asp	Leu	Gln	Leu	Gly	Gly	Glu	Gly	Thr	Leu	580	585	590
Tyr	Thr	Arg	Leu	Gly	Lys	Leu	Leu	Lys	Val	Asp	Gly	Thr	Ala	Met	Thr	595	600	605
Gly	Gly	Lys	Leu	Tyr	Met	Ser	Ala	Arg	Gly	Lys	Gly	Ala	Gly	Tyr	Leu	610	615	620
Asn	Arg	Thr	Gly	Gln	Arg	Val	Pro	Phe	Leu	Ser	Ala	Ala	Lys	Ile	Gly	625	630	635
Arg	Asp	Tyr	Ser	Phe	Phe	Thr	Asn	Ile	Glu	Thr	Asp	Gly	Gly	Leu	Leu	645	650	655
Ala	Ser	Leu	Asp	Ser	Val	Glu	Lys	Thr	Ala	Gly	Ser	Glu	Gly	Asp	Thr	660	665	670
Leu	Ser	Tyr	Tyr	Val	Arg	Arg	Gly	Asn	Ala	Ala	Arg	Thr	Ala	Ser	Ala	675	680	685
Ala	Ala	His	Ser	Ala	Pro	Ala	Gly	Leu	Lys	His	Ala	Val	Glu	Gln	Gly	690	695	700
Gly	Ser	Asn	Leu	Glu	Asn	Leu	Met	Val	Glu	Leu	Asp	Ala	Ser	Glu	Ser	705	710	715
Ser	Ala	Thr	Pro	Glu	Thr	Val	Glu	Thr	Ala	Ala	Ala	Asp	Arg	Thr	Asp	725	730	735
Met	Pro	Gly	Ile	Arg	Pro	Tyr	Gly	Ala	Thr	Phe	Arg	Ala	Ala	Ala	Ala	740	745	750

008304133-081604

Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu
755 760 765

Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln
770 775 780

Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr
785 790 795 800

Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu
805 810 815

Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly
820 825 830

Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly
835 840 845

Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp
850 855 860

Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly
865 870 875 880

Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser
885 890 895

Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr
900 905 910

Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala
915 920 925

Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys
930 935 940

Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn
945 950 955 960

Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser
965 970 975

Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu
980 985 990

Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly
995 1000 1005

Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr
1010 1015 1020

Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp
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His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe
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<213> Neisseria meningitidis

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gca ggt tgc ggc tca atc aat aat gta acc gtt tcc gac cag aaa ctt 96
Ala Gly Cys Gly Ser Ile Asn Asn Val Thr Val Ser Asp Gln Lys Leu
             20             25             30

cag gaa cgt gcc gcg ttt gcc ttg ggc gtc agc caa aat gcc gta aaa 144
Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys
             35             40             45

atc agc aac cgc agc aat gaa agc ata cgc atc aac ttt acc gca act 192
Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr
             50             55             60

gtg ggt aag cgc gtg agc caa tgc tat gtt acc agt gta atc agc aca 240
Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr
             65             70             75             80

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Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Gly Thr His
             85             90             95

aaa ggc aaa agt caa tgc aat gct ttg ctt aaa gcg gca ggc cgt tgc 336
Lys Gly Lys Ser Gln Cys Asn Ala Leu Leu Lys Ala Ala Gly Arg Cys
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<213> Neisseria meningitidis

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Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys
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Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr

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Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr				
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Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Gly Thr His				
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ctg ctg acg gaa aaa gtg tgc ccc atc atc gca tta atc ttg gtg ccg	96
Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro	
20 25 30	
ctg ttt ggg gcg ttg ctg gcg ggg ttt gat gta tcc caa tta aaa gaa	144
Leu Phe Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu	
35 40 45	
ttt tat tgc ggc ggc acc aaa tgc gtg atg cag att gtg att atg ttt	192
Phe Tyr Ser Gly Gly Thr Lys Ser Val Met Gln Ile Val Ile Met Phe	
50 55 60	
atg ttt tcc att ttg ttt gga atc atg aac gat gtg ggg ctg ttc	240
Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe	
65 70 75 80	
cgt ccg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg	288
Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val	
85 90 95	
gca gtg agt gtg ggg acg gtc ttg gtg tgc gtg ggc cag ttg gac	336
Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp	
100 105 110	
ggg gcg ggt gcg acg acg ttt tta ttg gtc gtc ccc gcc ctt ttg ccg	384
Gly Ala Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro	
115 120 125	
ctt tac aag cgt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg	432
Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu	
130 135 140	
act tcc agt gcg gga ttg att aac ctt ctg ccg tgg ggc ggg ccg acc	480

09830433 081601

Thr	Ser	Ser	Ala	Gly	Leu	Ile	Asn	Leu	Leu	Pro	Trp	Gly	Gly	Pro	Thr	
145					150					155					160	
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Gly	Arg	Val	Ala	Ser	Val	Leu	Gly	Ala	Asp	Val	Gly	Glu	Leu	Tyr	Lys	
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cct	ttg	ttg	acg	gtg	caa	att	atc	ggc	gtg	gtg	ttt	atc	ctt	gcg	ctg	576
Pro	Leu	Leu	Thr	Val	Gln	Ile	Ile	Gly	Val	Val	Phe	Ile	Leu	Ala	Leu	
				180				185					190			
tcc	ctg	ctt	ttg	ggc	gtg	cgt	gaa	aaa	agg	cgg	att	gtc	cgg	gag	ttg	624
Ser	Leu	Leu	Leu	Gly	Val	Arg	Glu	Lys	Arg	Arg	Ile	Val	Arg	Glu	Leu	
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Gly	Ala	Leu	Pro	Ala	Val	Ala	Asp	Leu	Ile	Lys	Pro	Val	Pro	Leu	Ser	
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gaa	gaa	gaa	caa	aaa	ttg	gcg	cgt	ccg	aaa	ctg	ttt	tgg	tgg	aat	gtc	720
Glu	Glu	Glu	Gln	Lys	Leu	Ala	Arg	Pro	Lys	Leu	Phe	Trp	Trp	Asn	Val	
					230					235					240	
ctg	ctg	ttt	ttg	gcg	gcg	atg	agc	ctg	ctt	ttt	tcg	ggc	atc	ttc	ccg	768
Leu	Leu	Phe	Leu	Ala	Ala	Met	Ser	Leu	Leu	Phe	Ser	Gly	Ile	Phe	Pro	
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Pro	Gly	Tyr	Val	Phe	Met	Leu	Ala	Ala	Thr	Ala	Ala	Leu	Leu	Leu	Asn	
			260					265					270			
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Tyr	Arg	Ser	Pro	Gln	Glu	Gln	Met	Glu	Arg	Ile	Tyr	Ala	His	Ala	Gly	
			275				280					285				
ggc	gcg	gtg	atg	atg	gcg	tcc	att	att	ttg	gcg	gca	ggc	acg	ttt	ttg	912
Gly	Ala	Val	Met	Met	Ala	Ser	Ile	Ile	Leu	Ala	Ala	Gly	Thr	Phe	Leu	
			290			295					300					
ggg	att	ttg	aag	ggc	gcg	ggg	atg	ttg	gac	gcg	att	tcc	aaa	gac	att	960
Gly	Ile	Leu	Lys	Gly	Ala	Gly	Met	Leu	Asp	Ala	Ile	Ser	Lys	Asp	Ile	
				310					315					320		
gtg	cat	atc	ctg	ccg	gac	gcg	ctg	ctg	cct	tat	ctg	cat	att	gcc	atc	1008
Val	His	Ile	Leu	Pro	Asp	Ala	Leu	Leu	Pro	Tyr	Leu	His	Ile	Ala	Ile	
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ggc	gtg	ttg	ggc	att	ccg	ctt	gag	ttg	ggt	ttg	agt	acg	gac	gct	tat	1056
Gly	Val	Leu	Gly	Ile	Pro	Leu	Glu	Leu	Val	Leu	Ser	Thr	Asp	Ala	Tyr	
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tat	ttc	gga	ctg	ttt	ccg	att	gtg	gag	cag	att	acc	tcg	cag	gcg	ggc	1104
Tyr	Phe	Gly	Leu	Phe	Pro	Ile	Val	Glu	Gln	Ile	Thr	Ser	Gln	Ala	Gly	
			355				360					365				
gtg	gcg	ccc	gaa	gca	gca	ggc	tat	gcg	atg	ttg	atc	ggc	agt	atc	gtc	1152
Val	Ala	Pro	Glu	Ala	Ala	Gly	Tyr	Ala	Met	Leu	Ile	Gly	Ser	Ile	Val	
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ggc	act	ttt	ggt	acg	ccg	ctt	tcg	ccg	gct	ttg	tgg	atg	ggc	ttg	ggc	1200

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Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
 385 390 395 400
 ttg gcg aaa ttg tcg atg ggc aaa cac atc cgt tat tcg ttt ttt tgg 1248
 Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
 405 410 415
 gcg tgg ggt ttg tcg ctg gcg ata ttg gcc agt tcg ata gcg gca gga 1296
 Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly
 420 425 430
 atc gtg cct ctg ccg taa 1314
 Ile Val Pro Leu Pro
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 Leu Phe Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
 35 40 45
 Phe Tyr Ser Gly Gly Thr Lys Ser Val Met Gln Ile Val Ile Met Phe
 50 55 60
 Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe
 65 70 75 80
 Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val
 85 90 95
 Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
 100 105 110
 Gly Ala Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro
 115 120 125
 Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
 130 135 140
 Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Trp Gly Gly Pro Thr
 145 150 155 160
 Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys
 165 170 175
 Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Ala Leu
 180 185 190
 Ser Leu Leu Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu
 195 200 205

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Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Val Pro Leu Ser
 210 215 220

Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val
 225 230 235 240

Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro
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Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn
 260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
 275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu
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Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Ile
 305 310 315 320

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
 325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr
 340 345 350

Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly
 355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val
 370 375 380

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
 385 390 395 400

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
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Ile Val Pro Leu Pro
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act tat ctg tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat 96
Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn
      20              25              30

ctc gaa gcc gca tct tgt aaa tat atc aac gag ata tac caa cga gca 144
Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala
      35              40              45

gac cca acc gca ccg ctg ttt cat ctg cgt aaa aaa ggc gca atc gtt 192
Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val
      50              55              60

cct aaa gaa gaa tac gtc gaa agt ttc gac gat ttg ggc aaa act cgc 240
Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg
      65              70              75              80

tac cgt ttt att aaa tcc gtt atc tac gaa cat atg aag aat ggt gcg 288
Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala
      85              90              95

tcg tta gtc tat aac cat att aac aac gag ccg ttt tca gac cat atc 336
Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
      100             105             110

gcc cgt caa gtc gcc cgc ttt gcc ggc gca cat act att gtt agt gga 384
Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly
      115             120             125

tat ctt gct ttt ggc agc gac gaa tct tat aaa aac cat tgg gat acc 432
Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr
      130             135             140

cgc gat gtg tat gcc atc cag ctt ttc ggc aag aaa cgt tgg caa ctt 480
Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu
      145             150             155             160

act gcc cct gat ttc cct atg cca ttg tat atg caa cag act aaa gat 528
Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp
      165             170             175

act gat att tcc att cct gaa cat atc gat atg gat att atc ctt gaa 576
Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu
      180             185             190

gca ggt gat gtc ctc tac atc cca cgc ggt tgg tgg cac aga cct atc 624
Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile
      195             200             205

ccg ctc ggc tgt gaa acc ttc cac ttc gct gtc ggt acc ttc ccg ccc 672
Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro
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aac ggc tat aat tac ctc gag tgg cta atg aag aaa ttc ccc acg ata 720
Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile
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Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val				
	260	265	270	
aat tac gaa gcc ttc agt gaa gac ttc ctc ggc aaa gaa cgc acc gat				864
Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp				
	275	280	285	
acc gct ttt cat ctc gaa cag ttc gcg aat ccc aac gct act ccg ctt				912
Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu				
	290	295	300	
tca gac gac gtc agg ttg aga cta aat gcc aat aat ttg gat acg ttg				960
Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu				
	305	310	315	320
gaa aag gga tat ttg att ggg aat ggg atg aag ata agc gta gat gaa				1008
Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu				
	325	330	335	
ttg ggg aaa aaa gtg tta gaa cac atc ggt aag aat gaa ccg tta ttg				1056
Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu				
	340	345	350	
ttg aaa aat cta ctg gtt aac ttc aat cag gga aaa cat gaa gaa gtt				1104
Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val				
	355	360	365	
agg aag ttg att tat cag ttg ata gag tta gat ttt ctg gaa ctt ttg				1152
Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Leu Leu				
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 35 40 45
 Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val
 50 55 60
 Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg
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 Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala
 85 90 95

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Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
100 105 110

Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly
115 120 125

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr
130 135 140

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu
145 150 155 160

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp
165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu
180 185 190

Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile
195 200 205

Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro
210 215 220

Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile
225 230 235 240

Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg
245 250 255

Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val
260 265 270

Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp
275 280 285

Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu
290 295 300

Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu
305 310 315 320

Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu
325 330 335

Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu
340 345 350

Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val
355 360 365

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cgc caa acc agc ctg acg ggt aaa gtg att ctg aca cga ccg ttg tca 96
 Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser
 20 25 30

ttt tcc cta tgg acg aca ttt gca tcg ata tct gcg tta ttg att atc 144
Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile
35 40 45

ctg ttt ttg ata ttt ggt aac tat acg cga aag aca aca gtg gag gga 192
Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly
50 55 60

caa att tta cct gca tcg ggc gta atc agg gtg tat gca ccg gat acg 240
Gln Ile Leu .Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr
65 70 75 80

ggg aca att aca gcg aaa ttc gtg gaa gat gga gaa aag gtt aag gct 288
Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala
85 90 95

ggc gac aag cta ttt gcg ctt tcg acc tca cgt ttc ggc gca gga gat 336
Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp
100 105 110

agc gtg cag cag cag ttg aaa acg gag gca gtt ttg aag aaa acg ttg 384
Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu
115 120 125

gca gaa cag gaa ctg ggt cgt ctg aag ctg ata cac ggg aat gaa acg 432
Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr
130 135 140

cgc agc ctt aaa gca act gtc gaa cgt ttg gaa aac cag aaa ctc cat 480
Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Lys Leu His
145 150 155 160

att tcg caa cag ata gac ggt cag aaa agg cgc att aga ctt gcg gaa 528
Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu
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gaa atg ttg cag aaa tat cgt ttc cta tcc gcc aat gat gca gtg cca 576
Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro
.180 .185 .190

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Lys.Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala
195 200 205

aaa ctt gat gcc tac cgc cga gaa gaa gtc ggg ctg ctt cag gaa atc 672
Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile
210 215 220

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Phe	Ser	Leu	Trp	Thr	Thr	Phe	Ala	Ser	Ile	Ser	Ala	Leu	Leu	Ile	Ile
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		115					120					125			
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	130					135					140				
Arg	Ser	Leu	Lys	Ala	Thr	Val	Glu	Arg	Leu	Glu	Asn	Gln	Lys	Leu	His
	145				150					155					160
Ile	Ser	Gln	Gln	Ile	Asp	Gly	Gln	Lys	Arg	Arg	Ile	Arg	Leu	Ala	Glu
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Glu	Met	Leu	Gln	Lys	Tyr	Arg	Phe	Leu	Ser	Ala	Asn	Asp	Ala	Val	Pro
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aat ctg aca ttg gcc agc ctc ccc aaa cgg cat gag aca gaa caa agc	144
Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser	
35 40 45	
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Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe	
50 55 60	
gaa atg cgc tct gaa caa atc atc cgt gca gga cgg tcg ggt tat ata	240
Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile	
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gca ata ccg aac gtc gaa gtc gga cag cag gtt gat cct tcc aaa ctg	288
Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu	
85 90 95	
ctc ttg agc att gtt ccc gaa cgt acc gag cta tat gcc cat cta tat	336
Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr	
100 105 110	
atc ccc agc agt gca gca ggc ttt atc aag ccg aaa gac aag gtt gtc	384
Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val	
115 120 125	
cta cgt tat cag gca tat ccc tat caa aaa ttc ggg ctt gct tcc ggc	432
Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly	
130 135 140	
agt gtc gta tca gta gca aaa acg gca ctg ggc aga cag gaa ttg tcg	480
Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser	
145 150 155 160	
gga ttg ggc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt	528
Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val	
165 170 175	
tat ctc gtg aaa ata aaa ccc gac aaa cca acc atc act gca tac ggt	576
Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly	
180 185 190	
gag gaa aaa ccg ctg caa atc ggc atg acg ttg gaa gca gac atc ctg	624
Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu	
195 200 205	
cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag ctg att tat agt	672
His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser	
210 215 220	
atg tcg ggc aaa ctg taa	690
Met Ser Gly Lys Leu	
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<210> 18
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 35 40 45
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
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 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
 65 70 75 80
 Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu
 85 90 95
 Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
 100 105 110
 Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
 115 120 125
 Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
 130 135 140
 Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
 145 150 155 160
 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
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 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
 180 185 190
 Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
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 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser
 210 215 220
 Met Ser Gly Lys Leu
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 <212> DNA
 <213> Neisseria meningitidis

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<221> CDS

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1 5 10 15

ccc ctt aaa acc tta gct gcc gat gaa aac gat gca gaa ctt atc cgt 96
Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg
20 25 30

tcc atg cag cgt cag cag cac ata gat gct gaa ttg tta act gat gca 144
 Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala
 35 40 45

aat gtc cgt ttc gag caa cca ttg gag aag aac aat tat gtc ctg agt 192
Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser
50 55 60

Gaa gat gaa aca cgg tgt act cgg gta aat tac att agt tta gat gat 240
Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp
65 70 75 80

aag acg gcg cgc aaa ttt tct ttt ctt cct tct gtg ctc atg aaa gaa 288
Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu
85 90 95

aca gct ttt aaa act ggg atg tgt tta ggt tcc aat aat ttg agc agg 336
Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg
100 105 110

cta caa aaa gcc gcg caa cag ata ctg att gtg cgt ggc tac ctc act 384
Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr
115 120 125

tcc caa gct att atc caa cca cag aat atg gat tcc gga att ctg aaa 432
Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys
130 135 140

tta	cgg	gta	tca	gca	ggc	gaa	atc	agg	gat	atc	cgc	tat	gaa	gaa	aaa	480
Leu	Arg	Val	Ser	Ala	Gly	Glu	Ile	Arg	Asp	Ile	Arg	Tyr	Glu	Glu	Lys	
145					150					155					160	

cgg gat gcg aag tct gcc gag ggc agt att agt gca ttc aat aac aaa 528
 Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys
 165 170 175

ctt ccc tta tat agg aac aaa att ctc aat ctt cgc gat gta gag cag 576

Leu	Pro	Leu	Tyr	Arg	Asn	Lys	Ile	Leu	Asn	Leu	Arg	Asp	Val	Glu	Gln		
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ggc	ttg	gaa	aac	ctg	cgt	cgt	ttg	cgg	agt	gtt	aaa	aca	gat	att	cag	624	
Gly	Leu	Glu	Asn	Leu	Arg	Arg	Leu	Pro	Ser	Val	Lys	Thr	Asp	Ile	Gln		
		195					200				205						
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Ile	Ile	Pro	Ser	Glu	Glu		Gly	Lys	Ser	Asp	Leu	Gln	Ile	Lys	Trp		
		210				215					220						
cag	cag	aat	aaa	ccc	ata	cgg	ttc	agt	atc	ggc	ata	gat	gat	gcg	ggc	720	
Gln	Gln	Asn	Lys	Pro	Ile	Arg	Phe	Ser	Ile	Gly	Ile	Asp	Asp	Ala	Gly		
225					230					235					240		
ggc	aaa	acg	acc	ggc	aaa	tat	caa	gga	aat	gtc	gct	tta	tcg	tcc	gat	768	
Gly	Lys	Thr	Thr	Gly	Lys	Tyr	Gln	Gly	Asn	Val	Ala	Leu	Ser	Ser	Asp		
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aac	cct	ttg	ggc	tta	agc	gat	tcg	ttt	tat	gtt	tca	tat	gga	cgc	ggc	816	
Asn	Pro	Leu	Gly	Leu	Ser	Asp	Ser	Phe	Tyr	Val	Ser	Tyr	Gly	Arg	Gly		
		260					265						270				
ttg	gtg	cac	aaa	acg	gac	ttg	act	gct	gcc	acc	ggc	acg	gaa	act	gaa	864	
Leu	Val	His	Lys	Thr	Asp	Leu	Thr	Ala	Ala	Thr	Gly	Thr	Glu	Thr	Glu		
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agc	gga	tcc	aga	agt	tac	agc	gtg	cat	tat	tcg	gtg	ccc	gta	aaa	aaa	912	
Ser	Gly	Ser	Arg	Ser	Tyr	Ser	Val	His	Tyr	Ser	Val	Pro	Val	Lys	Lys		
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tgg	ctg	ttt	tct	ttt	aat	cac	aat	gga	cat	cgt	tac	cac	gaa	gca	acc	960	
Trp	Leu	Phe	Ser	Phe	Asn	His	Asn	Gly	His	Arg	Tyr	His	Glu	Ala	Thr		
305					310					315					320		
gaa	ggc	tat	tcc	gtc	aat	tac	gat	tac	aac	ggc	aaa	caa	tat	cag	agc	1008	
Glu	Gly	Tyr	Ser	Val	Asn	Tyr	Asp	Tyr	Asn	Gly	Lys	Gln	Tyr	Gln	Ser		
				325				330					335				
agc	ctg	gcc	gcc	gag	cgc	atg	ctt	tgg	ccc	ccc	agc	ttt	cct	caa	act	1056	
Ser	Leu	Ala	Ala	Glu	Arg	Met	Leu	Trp	Pro	Pro	Ser	Phe	Pro	Gln	Thr		
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tca	gtc	cga	atg	aaa	tta	tgg	aca	cgc	caa	acc	tat	aaa	tac	atc	gac	1104	
Ser	Val	Arg	Met	Lys	Leu	Trp	Thr	Arg	Gln	Thr	Tyr	Lys	Tyr	Ile	Asp		
		355				360						365					
gat	gcc	gaa	atc	gaa	gtg	caa	cgc	cgc	cgc	tct	gca	ggc	tgg	gaa	gcc	1152	
Asp	Ala	Glu	Ile	Glu	Val	Gln	Arg	Arg	Arg	Ser	Ala	Gly	Trp	Glu	Ala		
	370					375					380						
gaa	ttg	cgc	cac	cgt	gct	tac	ctc	cac	cgt	tgg	cag	ctt	gac	ggc	aag	1200	
Glu	Leu	Arg	His	Arg	Ala	Tyr	Leu	His	Arg	Trp	Gln	Leu	Asp	Gly	Lys		
385					390					395					400		
ttg	tct	tac	aaa	cgc	ggg	acc	ggc	atg	cgc	caa	agt	atg	ccc	gca	cct	1248	
Leu	Ser	Tyr	Lys	Arg	Gly	Thr	Gly	Met	Arg	Gln	Ser	Met	Pro	Ala	Pro		
			405					410					415				
gaa	gaa	aac	ggc	ggc	ggc	ggt	act	att	cca	gcc	aca	tcc	cgt	atg	aaa	atc	1296

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Glu Glu Asn Gly Gly Gly Thr Ile Pro Ala Thr Ser Arg Met Lys Ile
 420 425 430

ata acc gcc gga ttg gat gca gcg gcc ccg tct atg ttg ggc aaa cag 1344
 Ile Thr Ala Gly Leu Asp Ala Ala Ala Pro Ser Met Leu Gly Lys Gln
 435 440 445

cag ttt ttc tac gca acc gcc att caa gct caa tgg aac aaa acg cct 1392
 Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro
 450 455 460

ttg gtt gcc caa gac aag ttg tct atc ggc agc cgc tac acc gtt cgc 1440
 Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg
 465 470 475 480

gga ttt gat ggg gag cag agt ctt ttc gga gag cga ggt ttc tac tgg 1488
 Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp
 485 490 495

cag aat act tta act tgg tat ttt cat ccg aac cat cag ttc tat ctc 1536
 Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu
 500 505 510

ggc gcg gac tat ggc cgc gta tct ggc gaa agt gca caa tat gta tcg 1584
 Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser
 515 520 525

ggc aag cag ctg atg ggt gca gtg gtc ggc ttc aga gga ggg cat aaa 1632
 Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys
 530 535 540

gta ggc ggt atg ttt gct tat gat ctg ttt gcc ggc aag ccg ctt cat 1680
 Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His
 545 550 555 560

aaa ccc aaa ggc ttt cag acg acc aac acc gtt tac ggc ttc aac ttg 1728
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aat tac agt ttc taa 1743
 Asn Tyr Ser Phe
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 <212> PRT
 <213> Neisseria meningitidis

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Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg
 20 25 30

Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala
 35 40 45

Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser

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50

55

60

Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp
65 70 75 80

Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu
85 90 95

Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg
100 105 110

Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr
115 120 125

Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys
130 135 140

Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys
145 150 155 160

Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys
165 170 175

Leu Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln
180 185 190

Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln
195 200 205

Ile Ile Pro Ser Glu Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp
210 215 220

Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly
225 230 235 240

Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Ser Asp
245 250 255

Asn Pro Leu Gly Leu Ser Asp Ser Phe Tyr Val Ser Tyr Gly Arg Gly
260 265 270

Leu Val His Lys Thr Asp Leu Thr Ala Ala Thr Gly Thr Glu Thr Glu
275 280 285

Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys Lys
290 295 300

Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr
305 310 315 320

Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser
325 330 335

Ser Leu Ala Ala Glu Arg Met Leu Trp Pro Pro Ser Phe Pro Gln Thr
340 345 350

Ser Val Arg Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp
355 360 365

Asp Ala Glu Ile Glu Val Gln Arg Arg Arg Ser Ala Gly Trp Glu Ala

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370	375	380
Glu Leu Arg His Arg	Ala Tyr Leu His Arg	Trp Gln Leu Asp Gly Lys
385	390	395 400
Leu Ser Tyr Lys Arg	Gly Thr Gly Met Arg	Gln Ser Met Pro Ala Pro
405	410	415
Glu Glu Asn Gly Gly Gly	Thr Ile Pro Ala Thr Ser Arg	Met Lys Ile
420	425	430
Ile Thr Ala Gly Leu Asp	Ala Ala Ala Pro Ser Met	Leu Gly Lys Gln
435	440	445
Gln Phe Phe Tyr Ala Thr	Ala Ile Gln Ala Gln Trp	Asn Lys Thr Pro
450	455	460
Leu Val Ala Gln Asp Lys	Leu Ser Ile Gly Ser Arg	Tyr Thr Val Arg
465	470	475 480
Gly Phe Asp Gly Glu Gln	Ser Leu Phe Gly Glu Arg	Gly Phe Tyr Trp
485	490	495
Gln Asn Thr Leu Thr Trp	Tyr Phe His Pro Asn His	Gln Phe Tyr Leu
500	505	510
Gly Ala Asp Tyr Gly Arg	Val Ser Gly Glu Ser Ala	Gln Tyr Val Ser
515	520	525
Gly Lys Gln Leu Met Gly	Ala Val Val Gly Phe Arg	Gly Gly His Lys
530	535	540
Val Gly Gly Met Phe Ala	Tyr Asp Leu Phe Ala Gly	Lys Pro Leu His
545	550	555 560
Lys Pro Lys Gly Phe Gln	Thr Thr Asn Thr Val Tyr	Gly Phe Asn Leu
565	570	575
Asn Tyr Ser Phe		
580		

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- <211> 411
- <212> DNA
- <213> Neisseria meningitidis
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- <221> CDS
- <222> (1) .. (408)

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ctt ttg ctt gtg tgg acg tgc ggt tac cga tac gcc gcc gac aag gcc 96
Leu Leu Leu Val Trp Thr Cys Gly Tyr Arg Tyr Ala Ala Asp Lys Ala
20 25 30

gaa gcg aaa caa acc gcc ctg att gcc acc tat cgg cat tct tct atg 144
Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met
35 40 45

gtt gcg gcg gaa caa tac gcc ttg cag ctt aaa aaa gcg cag gac gaa 192
Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu
50 55 60

agg cag cgg tgg tac gac ttt tcc caa aaa caa gga aga aag ccc gtg 240
Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val
65 70 75 80

aaa aaa cag tat ccg ccg caa acg aaa aaa gcc gcc tat ctg aaa acc 288
Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr
85 90 95

aag gaa gaa ctg ctt gcg gaa ttg gct tgc ctt aaa gcg gaa atg gct 336
Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala
100 105 110

gcc cta aaa aag ctc gat gcc tta atc tat ggg aaa gaa gtg cgg cag 384
Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln
115 120 125

aaa gaa cgc aac tcg tcg cag ggt taa 411
Lys Glu Arg Asn Ser Ser Gln Gly
130 135

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<210> 22
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<212> PRT
<213> Neisseria meningitidis

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09830433.081604

<400> 22

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Leu Leu Leu Val Trp Thr Cys Gly Tyr Arg Tyr Ala Ala Asp Lys Ala
20 25 30

Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met
35 40 45

Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu
50 55 60

Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val
65 70 75 80

Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr
85 90 95

Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala
100 105 110

Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln
115 120 125

Lys Glu Arg Asn Ser Ser Gln Gly
130 135

<210> 23

<211> 924

<212> DNA

<213> Neisseria meningitidis

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<222> (1) .. (921)

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aat aat ttc ggg ttt ttg cgc ctg ccg ctt aat ttt atg ccg tat gaa 96
Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
20 25 30

agt cat gcc gat tgg gtt att acc ggc gtg cct tat gat atg gcg gtt 144
Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
35 40 45

tca ggg cgt tcc ggc gcg cgt ttc ggt cct gaa gcc atc cgg cgc gcc 192
Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
50 55 60

tcc gtc aac ctc gct tgg gag cac cgc agg ttt cca tgg aca ttt gat 240
Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
65 70 75 80

gtg cgc gaa cgc ctg aac att att gat tgc ggc gac ttg gtt ttt tct 288
Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
85 90 95

ttt ggc gac agc agg gat ttt gtc gaa aaa atg gaa gcg cac gcc ggc 336
Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
100 105 110

aaa tta ctt tct tcc ggc aaa cgc tgt ttg agt ttg ggc ggc gac cat 384
Lys Leu Leu Ser Ser Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
115 120 125

ttc att acc ctc ccg ttg ttg cgc gcc cac gcc cgc tat ttc ggc aaa 432
Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
130 135 140

ctc gca ctg att cat ttt gac gcg cac acc gac acc tac gac aac ggc 480
Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
145 150 155 160

agc gaa tac gac cac ggt acg atg ttc tat acc gcc ccc aag gaa ggc 528
Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
165 170 175

ctc atc gac ccg tcc cgt tcc gta caa atc ggc ata cgt acc gaa cac 576

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Ser	Lys	Lys	Leu	Pro	Phe	Thr	Val	Leu	Thr	Ala	Pro	Gln	Val	Asn	Glu		
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gac	agt	gtt	gaa	gag	acc	gtc	cgt	aaa	atc	aaa	gaa	acc	gtc	ggc	aat	672	
Asp	Ser	Val	Glu	Glu	Thr	Val	Arg	Lys	Ile	Lys	Glu	Thr	Val	Gly	Asn		
		210				215					220						
atg	ccc	gtt	tac	ctg	act	ttc	gac	ata	gac	tgc	ctc	gac	ccg	tcg	ttc	720	
Met	Pro	Val	Tyr	Leu	Thr	Phe	Asp	Ile	Asp	Cys	Leu	Asp	Pro	Ser	Phe		
					230					235					240		
gcc	ccc	ggg	acc	ggg	acg	ccc	gta	tgc	ggc	ggc	ttg	agc	agc	gac	agg	768	
Ala	Pro	Gly	Thr	Gly	Thr	Pro	Val	Cys	Gly	Gly	Leu	Ser	Ser	Asp	Arg		
				245					250					255			
gca	tta	aaa	atc	cta	cgt	ggg	ctg	acg	gat	ctc	gac	atc	gtc	ggg	atg	816	
Ala	Leu	Lys	Ile	Leu	Arg	Gly	Leu	Thr	Asp	Leu	Asp	Ile	Val	Gly	Met		
			260					265					270				
gat	gtt	gta	gaa	gtt	gcc	ccc	tct	tac	gac	caa	tcc	gac	att	acc	gct	864	
Asp	Val	Val	Glu	Val	Ala	Pro	Ser	Tyr	Asp	Gln	Ser	Asp	Ile	Thr	Ala		
		275					280					285					
ttg	gcc	ggc	gcc	aca	att	gcc	ttg	gaa	atg	ctt	tac	ctt	caa	ggg	gcg	912	
Leu	Ala	Gly	Ala	Thr	Ile	Ala	Leu	Glu	Met	Leu	Tyr	Leu	Gln	Gly	Ala		
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aaa	aag	gac	tga													924	
Lys	Lys	Asp															
		305															

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 Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
 35 40 45
 Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
 50 55 60
 Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
 65 70 75 80
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 85 90 95

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att ccc tac ccc gtc acc agg cgg att gcc tca agt ttg tat tcc acc 96
Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr
20 25 30

gaa tat ttt gtc gta tgc ttt ctg cgt ttg atg cca ctc tct ccg tgt 144
Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys
35 40 45

aat ctg tat ttt gtc acc cat ctg cgt acc aat gaa tcc gaa ata gaa 192
Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu
50 55 60

aga tgg tct gct gtt ccc tgc caa ata gta ttg aac gac ggc aag tcc 240
Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser
65 70 75 80

gaa ttc ggc gga ttc gca ttt gaa gtg caa ctt tcc cta aca gaa aaa 288
Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
85 90 95

ggc cag tat gcg gta gca tac gac ctt tcc tgc aag aaa gat tgc cat 336
Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
100 105 110

gag cta cac gca act gac cca agg cga acg ata cca cat cca ata cct 384
Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro
115 120 125

gtc ccg cca ctg cac cgt cac cga aat cgc caa aca gct taa 426
Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala
130 135 140

<210> 26
<211> 141
<212> PRT
<213> Neisseria meningitidis

09830433-081604

<400> 26

Met	Glu	Gln	Ser	Gly	Lys	Phe	Ser	Trp	Ser	Ala	Ala	Ala	Phe	Trp	Asp
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Ile	Pro	Tyr	Pro	Val	Thr	Arg	Arg	Ile	Ala	Ser	Ser	Leu	Tyr	Ser	Thr
			20					25					30		
Glu	Tyr	Phe	Val	Val	Cys	Phe	Leu	Arg	Leu	Met	Pro	Leu	Ser	Pro	Cys
		35					40					45			
Asn	Leu	Tyr	Phe	Val	Thr	His	Leu	Arg	Thr	Asn	Glu	Ser	Glu	Ile	Glu
	50					55					60				
Arg	Trp	Ser	Ala	Val	Pro	Cys	Gln	Ile	Val	Leu	Asn	Asp	Gly	Lys	Ser
	65				70					75					80
Glu	Phe	Gly	Gly	Phe	Ala	Phe	Glu	Val	Gln	Leu	Ser	Leu	Thr	Glu	Lys
				85					90					95	
Gly	Gln	Tyr	Ala	Val	Ala	Tyr	Asp	Leu	Ser	Cys	Lys	Lys	Asp	Cys	His
			100					105					110		
Glu	Leu	His	Ala	Thr	Asp	Pro	Arg	Arg	Thr	Ile	Pro	His	Pro	Ile	Pro
		115					120					125			
Val	Pro	Pro	Leu	His	Arg	His	Arg	Asn	Arg	Gln	Thr	Ala			
	130					135					140				

<210> 27

<211> 351

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1) .. (348)

09030433-081604

<400> 27

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Met Gln Asn Gly Gly Gly Lys Ile Tyr Gln Thr Ala Asp Asn Val Glu
1 5 10 15

ggg att atg ctg ttg aag gta gta cct gag cgt acc gtt tcg gca gat 96
Gly Ile Met Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp
20 25 30

gca aaa acc aga gac ccg atg tgg gac aat gcg gct tta cag acc agc 144
Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser
35 40 45

gaa ggc gta aat ttt att gct cgt ttc cta gga ttt ttt agc gat ggg 192
Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly
50 55 60

gaa tac cgc tat gtg gat gtc ctg caa ccc aac cat tcc gat att att 240
Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
65 70 75 80

cgg tat tca ggt aaa gat ttt ccg cta aat caa ata ctt aac cat ata 288
Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile
85 90 95

cac ccc gcc cgt tat gcg gta acg ttc gaa aac aat gtc gat tcc aag 336
His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys
100 105 110

ctg cgc agg cac tga 351
Leu Arg Arg His
115

<210> 28

<211> 116

<212> PRT

<213> Neisseria meningitidis

<400> 28

Met Gln Asn Gly Gly Gly Lys Ile Tyr Gln Thr Ala Asp Asn Val Glu
1 5 10 15

Gly Ile Met Leu Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp
20 25 30

093043-08430

Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser
 35 40 45
 Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly
 50 55 60
 Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
 65 70 75 80
 Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile
 85 90 95
 His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys
 100 105 110
 Leu Arg Arg His
 115

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 <213> Neisseria meningitidis

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 <222> (1)..(1401)

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 1 5 10 15
 tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tcg gct atg 96
 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30
 aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144
 Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35 40 45
 cca cta tcc ctt tcc cca tcc gtt tcg gct ttt acg ctg cct gaa gca 192
 Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
 50 55 60
 tgg cgg gcg gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac 240
 Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80
 cag cgt gat gca gtg cgc gca cgg caa caa caa gcc aag gcc gca ttc 288
 Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
 85 90 95
 ctt ccc cat gta tcc gcc aat gcc agc tac cag cgc cag ccg cca tcg 336
 Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
 100 105 110
 att tct tcc acc cgc gaa aca cag gga tgg agc gtg cag gtg gga caa 384

09830433-081601

Ile	Ser	Thr	Arg	Glu	Thr	Gln	Gly	Trp	Ser	Val	Gln	Val	Gly	Gln		
	115					120					125					
acc	tta	ttt	gac	gct	gcc	aaa	ttt	gca	caa	tac	cgc	caa	agc	agg	ttc	432
Thr	Leu	Phe	Asp	Ala	Ala	Lys	Phe	Ala	Gln	Tyr	Arg	Gln	Ser	Arg	Phe	
	130					135					140					
gat	acg	cag	gct	gca	gaa	cag	cgt	ttc	gat	gcg	gca	cgc	gaa	gaa	ttg	480
Asp	Thr	Gln	Ala	Ala	Glu	Gln	Arg	Phe	Asp	Ala	Ala	Arg	Glu	Glu	Leu	
	145				150					155					160	
ctg	ttg	aaa	gtt	gcc	gaa	agt	tat	ttc	aac	gtt	tta	ctc	agc	cga	gac	528
Leu	Leu	Lys	Val	Ala	Glu	Ser	Tyr	Phe	Asn	Val	Leu	Leu	Ser	Arg	Asp	
				165					170					175		
acc	gtt	gcc	gcc	cat	gcg	gcg	gaa	aaa	gag	gct	tat	gcc	cag	cag	gta	576
Thr	Val	Ala	Ala	His	Ala	Ala	Glu	Lys	Glu	Ala	Tyr	Ala	Gln	Gln	Val	
				180				185					190			
agg	cag	gcg	cag	gct	tta	ttc	aat	aaa	ggc	gct	gcc	acc	gcg	ctg	gat	624
Arg	Gln	Ala	Gln	Ala	Leu	Phe	Asn	Lys	Gly	Ala	Ala	Thr	Ala	Leu	Asp	
		195					200					205				
att	cac	gaa	gcc	aaa	gcc	ggc	tac	gac	aat	gcc	ctg	gcc	caa	gaa	atc	672
Ile	His	Glu	Ala	Lys	Ala	Gly	Tyr	Asp	Asn	Ala	Leu	Ala	Gln	Glu	Ile	
		210				215					220					
gcc	gta	ttg	gct	gag	aaa	caa	acc	tat	gaa	aac	cag	ttg	aac	gac	tac	720
Ala	Val	Leu	Ala	Glu	Lys	Gln	Thr	Tyr	Glu	Asn	Gln	Leu	Asn	Asp	Tyr	
					230					235					240	
acc	gac	ctg	gat	agc	aaa	caa	atc	gag	gcc	ata	gat	acc	gcc	aac	ctg	768
Thr	Asp	Leu	Asp	Ser	Lys	Gln	Ile	Glu	Ala	Ile	Asp	Thr	Ala	Asn	Leu	
				245					250					255		
ttg	gca	cgc	tat	ctg	ccc	aag	ctg	gaa	cgt	tac	agt	ctg	gat	gaa	tgg	816
Leu	Ala	Arg	Tyr	Leu	Pro	Lys	Leu	Glu	Arg	Tyr	Ser	Leu	Asp	Glu	Trp	
			260					265					270			
cag	cgc	att	gcc	tta	tcc	aac	aat	cat	gaa	tac	cgg	atg	cag	cag	ctt	864
Gln	Arg	Ile	Ala	Leu	Ser	Asn	Asn	His	Glu	Tyr	Arg	Met	Gln	Gln	Leu	
		275					280					285				
gcc	ctg	caa	agc	agc	gga	cag	gcg	ctt	cgg	gca	gca	cag	aac	agc	cgc	912
Ala	Leu	Gln	Ser	Ser	Gly	Gln	Ala	Leu	Arg	Ala	Ala	Gln	Asn	Ser	Arg	
		290				295				300						
tat	ccc	acc	gtt	tct	gcc	cat	gtc	ggc	tat	cag	aat	aac	ctc	tac	act	960
Tyr	Pro	Thr	Val	Ser	Ala	His	Val	Gly	Tyr	Gln	Asn	Asn	Leu	Tyr	Thr	
					310				315						320	
tca	tct	gcg	cag	aat	aat	gac	tac	cac	tat	cgg	ggc	aaa	ggg	atg	agc	1

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
 355 360 365

ctg acc gca acc gag cgg cac atc aaa ctc gcc gta cgc cag gct tat 1152
 Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
 370 375 380

acc gaa agc ggt gcg gcg cgt tac caa atc atg gcg caa gaa cgg gtt 1200
 Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
 385 390 395 400

ttg gaa agc agc cgt ttg aaa ctg aaa tgc acc gaa acc ggc caa caa 1248
 Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
 405 410 415

tac ggc atc cgc aac cgg ctg gaa gta ata cgg gcg cgg cag gaa gtc 1296
 Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
 420 425 430

gcc caa gca gaa cag aaa ctg gct caa gca cgg tat aaa ttc atg ctg 1344
 Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
 435 440 445

gct tat ttg cgc ttg gtg aaa gag agc ggg tta ggg ttg gaa atg gta 1392
 Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
 450 455 460

ttt gcg gaa taa 1404
 Phe Ala Glu
 465

<210> 30
 <211> 467
 <212> PRT
 <213> Neisseria meningitidis

<400> 30
 Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
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Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
 50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
 85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
 100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln

009780-EE402860

115	120	125
Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe 130 135 140		
Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu 145 150 155 160		
Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp 165 170 175		
Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val 180 185 190		
Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp 195 200 205		
Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile 210 215 220		
Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr 225 230 235 240		
Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu 245 250 255		
Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp 260 265 270		
Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu 275 280 285		
Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg 290 295 300		
Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr 305 310 315 320		
Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser 325 330 335		
Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser 340 345 350		
Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln 355 360 365		
Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr 370 375 380		
Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val 385 390 395 400		
Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln 405 410 415		
Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val 420 425 430		
Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu		

0980433-081604

445

Phe Ala Glu
465

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<220>
<221> CDS
<222> (1) .. (693)
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 Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser
 165 170 175

gat aaa gat ttg cga gaa cct gat gcc ggc ctg ttg ttg aat att ttc 576
 Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
 180 185 190

gac ctg tat tac gat ttg gct tcc gcg ccg gca cca ata tgt cgc caa 624
 Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln
 195 200 205

gcg cgc cca cat ttc gga agc agc aaa aaa agc gtc aac atg gca tat 672
 Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr
 210 215 220

ccg tca tgt tgc gcc caa gta taa 696
 Pro Ser Cys Cys Ala Gln Val
 225 230

<210> 32
 <211> 231
 <212> PRT
 <213> Neisseria meningitidis

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 Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn
 1 5 10 15

Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
 20 25 30

Ala Ser Gly Tyr His Leu Glu Tyr Gln Tyr Gly Tyr Arg Tyr Ser Ala
 35 40 45

Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
 50 55 60

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
 65 70 75 80

Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
 85 90 95

Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
 100 105 110

Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
 115 120 125

Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe
 130 135 140

Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
 145 150 155 160

Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser
 165 170 175

00930433-081604

Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
 180 185 190
 Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln
 195 200 205
 Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr
 210 215 220
 Pro Ser Cys Cys Ala Gln Val
 225 230

<210> 33
 <211> 909
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1)..(906)

<400> 33
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 1 5 10 15
 acc aaa ggg ctg ttg ata aac ggt tac cat ttc acc gcc cac gcg acg 96
 Thr Lys Gly Leu Leu Ile Asn Gly Tyr His Phe Thr Ala His Ala Thr
 20 25 30
 aat ctt tgg ctg ccg cag act ttg ggg ctg cgg gga gag cgg aac aat 144
 Asn Leu Ser Leu Pro Gln Thr Leu Gly Leu Pro Gly Glu Pro Asn Asn
 35 40 45
 aac att gtc agc ttg gcg aag cag gcg ggt ttt cgg acg gcg tgg ctg 192
 Asn Ile Val Ser Leu Ala Lys Gln Ala Gly Phe Arg Thr Ala Trp Leu
 50 55 60
 tct aat caa gga atg ttg ggg cat ttt gcc aac gaa att tcc acc tat 240
 Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr
 65 70 75 80
 gcc cta cgc agc gat tat cgg tgg ttt acc caa agg ggt gat tat ggc 288
 Ala Leu Arg Ser Asp Tyr Pro Trp Phe Thr Gln Arg Gly Asp Tyr Gly
 85 90 95
 aaa agc gcg ggg ttg agc gac cgc ctt ttg ttg cgg gcg ttc aaa cgg 336
 Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Leu Pro Ala Phe Lys Arg
 100 105 110
 gtt ttg ata gga aat gca ggc acg aag cct cgg ctg att gtg atg cac 384
 Val Leu Ile Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His
 115 120 125
 ctg atg ggt tgg cac agt gat ttt tgc aca cgt ttg gat aag gat gcg 432
 Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala
 130 135 140

09830433 081604

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<210> 34
<211> 302
<212> PRT
<213> Neisseria meningitidis
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Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr

65	70	75	80
Ala Leu Arg Ser Asp Tyr Pro Trp Phe Thr Gln Arg Gly Asp Tyr Gly	85	90	95
Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Leu Pro Ala Phe Lys Arg	100	105	110
Val Leu Ile Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His	115	120	125
Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala	130	135	140
Arg Arg Phe Gln Tyr Gln Thr Glu Lys Ile Ser Cys Tyr Val Ser Thr	145	150	155
Ile Ala Gln Thr Asp Lys Phe Leu Glu Asp Thr Val Lys Ile Leu Asn	165	170	175
Glu Asn Lys Glu Ser Trp Ser Leu Val Tyr Phe Ser Asp His Gly Leu	180	185	190
Met His Val Gly Lys Gly Gly Glu Arg Thr Leu Thr His Gly Ala Trp	195	200	205
Lys Arg Gln Ser Tyr Gly Val Pro Leu Val Lys Ile Ser Ser Asp Asp	210	215	220
Thr Arg Arg Glu Met Ile Lys Val Arg Arg Ser Ala Phe Asn Phe Leu	225	230	235
Arg Gly Phe Gly Ser Trp Thr Gly Ile Glu Thr Asp Glu Leu Pro Asp	245	250	255
Asp Gly Tyr Asp Phe Trp Gly Asn Val Pro Asp Val Gln Gly Glu Gly	260	265	270
Asn Asn Leu Ala Phe Ile Asp Gly Leu Pro Asp Asp Pro Ala Pro Trp	275	280	285
Tyr Ala Gly Lys Gly Lys Ser Thr Lys Asn Thr Ser Lys Lys	290	295	300

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 <212> DNA
 <213> Neisseria meningitidis

<220>
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 <222> (1) .. (861)

09830433-081601

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1 5 10 15

gaa tcg aat ccg ctt gcc gtc gcc ggt tgc gtc aat gct tat ttt gca 96
Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala
20 25 30

cga ttg gcc acc caa agc ggt ttc aaa gcc atc tat ctg tcc ggc ggc 144
Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly
35 40 45

ggc gtg gca gcc tgt tct tgc ggt atc cct gat ttg ggc att acc aca 152
Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr
50 55 60

atg gaa gat gtg ctg atc gac gca cga cgc att acg gac aac gtg gat 240
Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp
65 70 75 80

acg cct ctg ctg gtg gac atc gat gtg ggt tgg ggc ggt gca ttc aat 288
Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn
85 90 95

att gcc cgt acc att cgc aac ttt gaa cgc gcc ggt gtt gca gcg gtt 336
Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val
100 105 110

cac atc gaa gat cag gta ggc caa aaa cgc tgc ggc cac cgt ccg aac 384
His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn
115 120 125

aaa gcc att gta tct aaa gat gaa atg gtc gac cgt atc aaa gct gcc 432
Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala
130 135 140

gta gat gcg cgc gtt gat gag aac ttc gtc att atg gcg cgt acc gat 480
Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp
145 150 155 160

gcg ctg gcg gta gaa ggt ttg gat gcc gct atc gaa cgt gcc caa gct 528
Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala
165 170 175

tgt gcc gaa gcc ggt gcg gac atg att ttc cct gaa gcc atg acc gat 576
Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Gly Ala Met Thr Asp
180 185 190

ttg aac atg tac cgc caa ttt gca gat gcg gtc aaa gtc ccc gtg ttg 624
Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu
195 200 205

gcg aac att acc gag ttt ggt tct acc ccg ctt tat acc caa agc gag 672
Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu
210 215 220

ctg gct gaa aac gcc gtg tcg ctg gtc cgc tat ccg ctg tca tcg ttc 720
Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe
225 230 235 240

cgt gca gca agc aaa gcc gct ctg aat gtt tac gaa gcg att atg cgc 768
Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg
245 250 255

09330433-081601

gat ggc act tca ggc ggc ggt ggt gga cag tat gca aac ccg tgc cga 816
Asp Gly Thr Ser Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg
260 265 270

gct gta cga gca tct gaa cta tca tgc ctt cga gca aaa act gga taa 864
Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly
275 280 285

<210> 36
<211> 287
<212> PRT
<213> Neisseria meningitidis

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20 25 30
Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly
35 40 45
Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr
50 55 60
Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp
65 70 75 80
Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn
85 90 95
Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val
100 105 110
His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn
115 120 125
Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala
130 135 140
Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp
145 150 155 160
Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala
165 170 175
Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Glu Ala Met Thr Asp
180 185 190
Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu
195 200 205
Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu
210 215 220
Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe
225 230 235 240

09043-001601

Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg
 245 250 255
 Asp Gly Thr Ser Gly Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg
 260 265 270
 Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly
 275 280 285

<210> 37
 <211> 921
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1)..(918)

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 5 10 15
 ctt tca gac tgc ctt tca aca aat ccg cat cgg tgg tct gaa aac ccg 96
 Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro
 20 25 30
 aaa ccc ata aaa aca caa agg aga aat acc atg act gaa act acc caa 144
 Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln
 35 40 45
 acc ccg acc ctc aaa cct aaa aaa tcc gtt gcg ctt tct ggc gtt gcg 192
 Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala
 50 55 60
 gcc ggt aat acc ggt ttg tgt acc gtt ggc cgt acc ggc aac gat ttg 240
 Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu
 65 70 75 80
 agc tat cgc ggt tac gac att ctg gat ttg gca caa aaa tgt gag ttt 288
 Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe
 85 90 95
 gaa gaa gtt gcc cac ctg ctg att cac ggc cat tta ccc aac aaa ttc 336
 Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe
 100 105 110
 gag ctg gcc gct tat aaa gcc aag ctt aaa tcc atg cgc ggc ctg cct 384
 Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro
 115 120 125
 atc cgt gtg att aaa gtt ttg gaa agc ctg cct gca cat acc cat ccg 432
 Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro
 130 135 140
 atg gac gtg atg cgt acc ggc gta tcc atg ctg ggc tgt gtt cat cct 480
 Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro
 145 150 155 160

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gaa cgt gaa ggc cat ccg gaa agc gaa gcg cgc gac att gcc gac aaa	528
Glu Arg Glu Gly His Pro Glu Ser Glu Ala Arg Asp Ile Ala Asp Lys	
165 170 175	
ctg atc gcc agc ctc ggc agt atc ctc ttg tac tgg tat caa tat tcg	576
Leu Ile Ala Ser Leu Gly Ser Ile Leu Leu Tyr Trp Tyr Gln Tyr Ser	
180 185 190	
cac aac ggc aaa cgc att gaa gtt gaa agc gaa gaa gag acc atc ggc	624
His Asn Gly Lys Arg Ile Glu Val Glu Ser Glu Glu Glu Thr Ile Gly	
195 200 205	
ggt cat ttc ctg cac ctg ttg cac ggc aaa cgc cca agc gaa tca cac	672
Gly His Phe Leu His Leu Leu His Gly Lys Arg Pro Ser Glu Ser His	
210 215 220	
atc aaa gcc atg cac gtt tca ctg att ctg tat gcc gaa cac gag ttc	720
Ile Lys Ala Met His Val Ser Leu Ile Leu Tyr Ala Glu His Glu Phe	
225 230 235 240	
aac gct tct acc ttt acc gcc cgc gtg atc gcc ggt aca ggc tct gat	768
Asn Ala Ser Thr Phe Thr Ala Arg Val Ile Ala Gly Thr Gly Ser Asp	
245 250 255	
atg tac tcc agc att acc gga gca atc ggc gcg ttg aaa ggt ccg aaa	816
Met Tyr Ser Ser Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Lys	
260 265 270	
cac ggc ggc gcg aac gaa ggg ctt acg ata ttc aaa aac gct acc gca	864
His Gly Gly Ala Asn Glu Gly Leu Thr Ile Phe Lys Asn Ala Thr Ala	
275 280 285	
atg ccg acg aag ccg aag ccg aca tcc gcg aac gca tgg gcc gca aag	912
Met Pro Thr Lys Pro Lys Pro Thr Ser Ala Asn Ala Ser Ala Ala Lys	
290 295 300	
aaa tgg tga	921
Lys Ser	
305	

<210> 38
 <211> 306
 <212> PRT
 <213> Neisseria meningitidis

<400> 38
 Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro
 1 5 10 15
 Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro
 20 25 30
 Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln
 35 40 45
 Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala
 50 55 60

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Ala	Gly	Asn	Thr	Ala	Leu	Cys	Thr	Val	Gly	Arg	Thr	Gly	Asn	Asp	Leu	65	70	75	80
Ser	Tyr	Arg	Gly	Tyr	Asp	Ile	Leu	Asp	Leu	Ala	Gln	Lys	Cys	Glu	Phe	85	90	95	
Glu	Glu	Val	Ala	His	Leu	Leu	Ile	His	Gly	His	Leu	Pro	Asn	Lys	Phe	100	105	110	
Glu	Leu	Ala	Ala	Tyr	Lys	Ala	Lys	Leu	Lys	Ser	Met	Arg	Gly	Leu	Pro	115	120	125	
Ile	Arg	Val	Ile	Lys	Val	Leu	Glu	Ser	Leu	Pro	Ala	His	Thr	His	Pro	130	135	140	
Met	Asp	Val	Met	Arg	Thr	Gly	Val	Ser	Met	Leu	Gly	Cys	Val	His	Pro	145	150	155	160
Glu	Arg	Glu	Gly	His	Pro	Glu	Ser	Glu	Ala	Arg	Asp	Ile	Ala	Asp	Lys	165	170	175	
Leu	Ile	Ala	Ser	Leu	Gly	Ser	Ile	Leu	Leu	Tyr	Trp	Tyr	Gln	Tyr	Ser	180	185	190	
His	Asn	Gly	Lys	Arg	Ile	Glu	Val	Glu	Ser	Glu	Glu	Glu	Thr	Ile	Gly	195	200	205	
Gly	His	Phe	Leu	His	Leu	Leu	His	Gly	Lys	Arg	Pro	Ser	Glu	Ser	His	210	215	220	
Ile	Lys	Ala	Met	His	Val	Ser	Leu	Ile	Leu	Tyr	Ala	Glu	His	Glu	Phe	225	230	235	240
Asn	Ala	Ser	Thr	Phe	Thr	Ala	Arg	Val	Ile	Ala	Gly	Thr	Gly	Ser	Asp	245	250	255	
Met	Tyr	Ser	Ser	Ile	Thr	Gly	Ala	Ile	Gly	Ala	Leu	Lys	Gly	Pro	Lys	260	265	270	
His	Gly	Gly	Ala	Asn	Glu	Gly	Leu	Thr	Ile	Phe	Lys	Asn	Ala	Thr	Ala	275	280	285	
Met	Pro	Thr	Lys	Pro	Lys	Pro	Thr	Ser	Ala	Asn	Ala	Ser	Ala	Ala	Lys	290	295	300	
Lys	Ser															305			

<210> 39
 <211> 945
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1)..(942)

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<400> 39

atg cac cta tgt gga aag tat tat gga gta aat atg aag ctg cgt gat	48
Met His Leu Cys Gly Lys Tyr Tyr Gly Val Asn Met Lys Leu Arg Asp	
1 5 10 15	
tta ctg atg gga ata ttc ttg gca gtt tct gcg gcc ctt ctg aat gca	96
Leu Leu Met Gly Ile Phe Leu Ala Val Ser Ala Ala Leu Leu Asn Ala	
20 25 30	
acc atc ggc ata ttc agc aag ata ttg atg gag cag ggc ttg tct gtt	144
Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val	
35 40 45	
cag cat att gca ttt ttg aaa act ttg aca ggt ttc gtg ttt atc agc	192
Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser	
50 55 60	
att ttg ctt tgc cgt acc ggt ttt acc aga cag att gcg gat att tca	240
Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser	
65 70 75 80	
aga aag aaa gag gca att ttg ccg ttg ctg tta aaa gta gca att tgt	288
Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Leu Lys Val Ala Ile Cys	
85 90 95	
gct ttt ttc gga att tat acg ttg ttt ttc ttt gaa acc aca gct tat	336
Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr	
100 105 110	
caa tat ggc aat gct gcg aat gta gta gtt gta tta atg gca tcg gct	384
Gln Tyr Gly Asn Ala Ala Asn Val Val Val Val Leu Met Ala Ser Ala	
115 120 125	
gcc gta tct gcc ttg ata ttg gac agc ata ctg tta gat gaa cgt att	432
Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile	
130 135 140	
tgc att tct tca gtc gtc ggt gtg ggt ttg gca gta ttg ggg atc gca	480
Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala	
145 150 155 160	
atg att tct tgg act gga gaa gga agt tta ggg ttg att ctg aat gcc	528
Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala	
165 170 175	
gca ctg gcg ggc tcg ggc tac ggt tgt ttt tcc gtt ttg att aag aaa	576
Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys	
180 185 190	
ttc ggc cta aac ggc ggt att tat ttg aca cgg ata ttg atg ttt ttt	624
Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe	
195 200 205	
gga agt att ttt ttg ttt atc cct tca ttg gaa ggt att gag gat ata	672
Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile	
210 215 220	
cat tgg caa tgg tct ttt att ccg cca ctc ttg gca ttg tct tta ttg	720
His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu	
225 230 235 240	

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ccg acg att tta gga ttt tat tgt aca act aaa gca ttg gat tat ttg	768
Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu	
245 250 255	
agt gct gcg aag gta cag gta act gaa ttg gcc gag cca ttg ttt gct	816
Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala	
260 265 270	
gcc gta ctg gct tgg ttg ttt ttg aat gaa ata ccg gaa gga cgc ttc	864
Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe	
275 280 285	
ttt gtc ggc gcc att ctg att att gcc ggt att gtg tct atc aat ggg	912
Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly	
290 295 300	
ctg tat cga cca ttg ttg aag cga att gaa taa	945
Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu	
305 310	

<210> 40
 <211> 314
 <212> PRT
 <213> Neisseria meningitidis

<400> 40
 Met His Leu Cys Gly Lys Tyr Tyr Gly Val Asn Met Lys Leu Arg Asp
 1 5 10 15
 Leu Leu Met Gly Ile Phe Leu Ala Val Ser Ala Ala Leu Leu Asn Ala
 20 25 30
 Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val
 35 40 45
 Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser
 50 55 60
 Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser
 65 70 75 80
 Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Lys Val Ala Ile Cys
 85 90 95
 Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr
 100 105 110
 Gln Tyr Gly Asn Ala Ala Asn Val Val Val Val Leu Met Ala Ser Ala
 115 120 125
 Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile
 130 135 140
 Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala
 145 150 155 160
 Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala
 165 170 175

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Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys
180 185 190

Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe
195 200 205

Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile
210 215 220

His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu
225 230 235 240

Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu
245 250 255

Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala
260 265 270

Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe
275 280 285

Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly
290 295 300

Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu
305 310

<210> 41
<211> 2610
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1) ... (2607)

<400> 41
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Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu
1 5 10 15

gaa tac tac gac gcg cgt gcg gcg tgt gag gac atc aag ccc ggc tct 96
Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser
20 25 30

tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144
Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
35 40 45

aac cgc gcg gac aaa gtc gat ttg ccg acg ctg caa agc tgg ctg ggt 192
Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
50 55 60

cag ctg att gag gga aaa cag gaa atc gac ttt cct tgg tat ccg gcg 240
Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
65 70 75 80

cgg gtg gtg tgc cac gat att ctg ggg cag acc gcg ttg gtg gat ttg 288

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Arg	Val	Val	Cys	His	Asp	Ile	Leu	Gly	Gln	Thr	Ala	Leu	Val	Asp	Leu			
85																90		
95																		
gca	ggt	ctg	cgc	gat	gcg	att	gcc	gaa	aaa	ggc	ggc	gat	cct	gcc	aaa	336		
Ala	Gly	Leu	Arg	Asp	Ala	Ile	Ala	Glu	Lys	Gly	Gly	Asp	Pro	Ala	Lys			
			100				105						110					
gtg	aat	ccg	gtg	gtt	gca	aaa	ccc	agc	ttc	atc	gtc	gac	cac	tct	ctg	384		
Val	Asn	Pro	Val	Val	Ala	Lys	Pro	Ser	Phe	Ile	Val	Asp	His	Ser	Leu			
			115				120						125					
gcc	gtt	gaa	tgc	ggc	ggc	tac	gac	ccc	gat	gcc	ttc	cgc	aaa	aac	cgc	432		
Ala	Val	Glu	Cys	Gly	Gly	Tyr	Asp	Pro	Asp	Ala	Phe	Arg	Lys	Asn	Arg			
			130				135						140					
caa	atc	gaa	gac	aga	cgt	aac	gaa	gac	cgt	ttc	cac	ttc	atc	aac	tgg	480		
Gln	Ile	Glu	Asp	Arg	Arg	Asn	Glu	Asp	Arg	Phe	His	Phe	Ile	Asn	Trp			
			145				150						160					
aca	aaa	acc	gca	ttt	gaa	aat	gtg	gac	gtg	att	ccg	gcg	ggc	aac	ggc	528		
Thr	Lys	Thr	Ala	Phe	Glu	Asn	Val	Asp	Val	Ile	Pro	Ala	Gly	Asn	Gly			
			165						170						175			
atc	atg	cac	caa	atc	aat	cta	gaa	aaa	atg	tgc	ccc	gtc	gtc	caa	gtc	576		
Ile	Met	His	Gln	Ile	Asn	Leu	Glu	Lys	Met	Ser	Pro	Val	Val	Gln	Val			
			180						185						190			
aaa	aac	ggc	gtg	gcg	ttc	ccc	gat	acc	tgc	gtc	ggc	acg	gat	tgc	cac	624		
Lys	Asn	Gly	Val	Ala	Phe	Pro	Asp	Thr	Cys	Val	Gly	Thr	Asp	Ser	His			
			195			200						205						
acg	ccg	cac	gtc	gat	gcg	ctg	ggc	gtg	att	tcc	gtg	ggc	gtg	ggc	gga	672		
Thr	Pro	His	Val	Asp	Ala	Leu	Gly	Val	Ile	Ser	Val	Gly	Val	Gly	Gly			
			210			215						220						
ttg	gaa	gcg	gaa	acc	gtg	atg	ctg	ggt	cgc	gcg	tcc	atg	atg	cgc	ctg	720		
Leu	Glu	Ala	Glu	Thr	Val	Met	Leu	Gly	Arg	Ala	Ser	Met	Met	Arg	Leu			
			225			230						235			240			
ccc	gat	att	gtc	ggc	gtt	gag	ctg	aac	ggc	aaa	cgg	cag	gcg	ggc	att	768		
Pro	Asp	Ile	Val	Gly	Val	Glu	Leu	Asn	Gly	Lys	Arg	Gln	Ala	Gly	Ile			
			245						250						255			
acg	gcg	acg	gat	att	gtg	ttg	gca	ctg	acc	gag	ttt	ctg	cgc	aaa	gaa	816		
Thr	Ala	Thr	Asp	Ile	Val	Leu	Ala	Leu	Thr	Glu	Phe	Leu	Arg	Lys	Glu			
			260			265						270						
cgc	gtg	gtc	ggg	gcg	ttt	gtc	gaa	ttc	ttc	ggc	gag	ggc	gcg	aga	agc	864		
Arg	Val	Val	Gly	Ala	Phe	Val	Glu	Phe	Phe	Gly	Glu	Gly	Ala	Arg	Ser			
			275			280						285						
ctg	tct	atc	ggc	gac	cgc	gcg	acc	att	tcc	aac	atg	acg	ccg	gag	ttc	912		
Leu	Ser	Ile	Gly	Asp	Arg	Ala	Thr	Ile	Ser	Asn	Met	Thr	Pro	Glu	Phe			
			290			295						300						
ggc	gcg	act	gcc	gcg	atg	ttc	gct	att	gat	gag	caa	acc	att	gat	tat	960		

Leu	Lys	Leu	Thr	Gly	Arg	Asp	Asp	Ala	Gln	Val	Lys	Leu	Val	Glu	Thr	
				325					330					335		
tac	gcc	aaa	acc	gca	ggc	tta	tgg	gca	gat	gcc	ttg	aaa	acc	gcc	gtt	1056
Tyr	Ala	Lys	Thr	Ala	Gly	Leu	Trp	Ala	Asp	Ala	Leu	Lys	Thr	Ala	Val	
				340					345					350		
tat	ccg	cgc	gtt	ttg	aaa	ttt	gat	ttg	agc	agc	gta	acg	cgc	aat	atg	1104
Tyr	Pro	Arg	Val	Leu	Lys	Phe	Asp	Leu	Ser	Ser	Val	Thr	Arg	Asn	Met	
				355					360					365		
gca	ggc	ccg	agc	aac	ccg	cac	gcg	cgt	ttt	gcg	acc	gcc	gat	ttg	gcc	1152
Ala	Gly	Pro	Ser	Asn	Pro	His	Ala	Arg	Phe	Ala	Thr	Ala	Asp	Leu	Ala	
				370					375					380		
agc	aaa	ggc	ttg	gct	aaa	cct	tac	gaa	gag	cct	tca	gac	ggc	caa	atg	1200
Ser	Lys	Gly	Leu	Ala	Lys	Pro	Tyr	Glu	Glu	Pro	Ser	Asp	Gly	Gln	Met	
				385					390					395		
ccc	gac	ggc	gcg	gtc	atc	atc	gcc	gcg	att	acc	agt	tgc	acc	aac	act	1248
Pro	Asp	Gly	Ala	Val	Ile	Ile	Ala	Ala	Ile	Thr	Ser	Cys	Thr	Asn	Thr	
				405					410					415		
tcc	aac	ccg	cgc	aac	gtt	gtt	gcc	gcc	gcg	ctc	ttg	gcg	cgc	aac	gcc	1296
Ser	Asn	Pro	Arg	Asn	Val	Val	Ala	Ala	Ala	Leu	Leu	Ala	Arg	Asn	Ala	
				420					425					430		
aac	tgc	ttc	ggg	ctg	aaa	cgc	aaa	ccg	tgg	gtc	aaa	acc	tgc	ttt	gcc	1344
Asn	Cys	Phe	Gly	Leu	Lys	Arg	Lys	Pro	Trp	Val	Lys	Thr	Ser	Phe	Ala	
				435					440					445		
ccc	ggt	tgc	aaa	gtg	gcg	gaa	att	tat	ttg	aaa	gaa	gca	ggc	ctg	ctg	1392
Pro	Gly	Ser	Lys	Val	Ala	Glu	Ile	Tyr	Leu	Lys	Glu	Ala	Gly	Leu	Leu	
				450					455					460		
ccc	gaa	atg	gaa	aaa	ctc	ggc	ttc	ggt	atc	gtc	gcc	ttc	gcc	tgc	acc	1440
Pro	Glu	Met	Glu	Lys	Leu	Gly	Phe	Gly	Ile	Val	Ala	Phe	Ala	Cys	Thr	
				465					470					475		
acc	tgc	aac	ggc	atg	agt	ggc	gcg	ctg	gat	ccg	aaa	atc	cag	aaa	gaa	1488
Thr	Cys	Asn	Gly	Met	Ser	Gly	Ala	Leu	Asp	Pro	Lys	Ile	Gln	Lys	Glu	
				485					490					495		
atc	atc	gac	cgc	gat	ttg	tac	gcc	acc	gcc	gta	tta	tca	ggc	aac	cgc	1536
Ile	Ile	Asp	Arg	Asp	Leu	Tyr	Ala	Thr	Ala	Val	Leu	Ser	Gly	Asn	Arg	
				500					505					510		
aac	ttc	gac	ggc	cgt	gtc	cat	ccg	tat	gcg	aaa	cag	gct	ttc	ctc	gct	1584
Asn	Phe	Asp	Gly	Arg	Val	His	Pro	Tyr	Ala	Lys	Gln	Ala	Phe	Leu	Ala	
				515					520					525		
tgc	cct	ccg	ttg	gtc	gtt	gcc	tac	gcg	ctg	gca	ggc	agt	atc	cgt	ttc	1632
Ser	Pro	Pro	Leu	Val	Val	Ala	Tyr	Ala	Leu	Ala	Gly	Ser	Ile	Arg	Phe	
				530					535					540		
gat	att	gaa	aac	gac	gta	ctc	ggc	gtt	gca	gac	ggc	aag	gaa	atc	cgc	1680
Asp	Ile	Glu	Asn	Asp	Val	Leu	Gly	Val	Ala	Asp	Gly	Lys</				

Leu	Lys	Asp	Ile	Trp	Pro	Ala	Asp	Glu	Glu	Ile	Asp	Ala	Val	Val	Ala				
																565	570	575	
gaa	tat	gtg	aaa	ccg	cag	cag	ttc	cgc	gat	gtg	tat	gta	ccg	atg	ttc	1776			
Glu	Tyr	Val	Lys	Pro	Gln	Gln	Phe	Arg	Asp	Val	Tyr	Val	Pro	Met	Phe				
																580	585	590	
gac	acc	ggc	aca	gcg	caa	aaa	gca	cct	agt	ccg	ctg	tac	gat	tgg	cgt	1824			
Asp	Thr	Gly	Thr	Ala	Gln	Lys	Ala	Pro	Ser	Pro	Leu	Tyr	Asp	Trp	Arg				
																595	600	605	
ccg	atg	tcc	acc	tac	atc	cgc	cgt	ccg	cct	tac	tgg	gaa	ggc	gcg	ctg	1872			
Pro	Met	Ser	Thr	Tyr	Ile	Arg	Arg	Pro	Pro	Tyr	Trp	Glu	Gly	Ala	Leu				
																610	615	620	
gca	ggg	gaa	cgc	aca	tta	aga	ggc	atg	cgt	ccg	ctg	gcg	att	ttg	ccc	1920			
Ala	Gly	Glu	Arg	Thr	Leu	Arg	Gly	Met	Arg	Pro	Leu	Ala	Ile	Leu	Pro				
																625	630	635	640
gac	aac	atc	acc	acc	gac	cac	ctc	tgc	ccg	tcc	aat	gcg	att	ttg	gcc	1968			
Asp	Asn	Ile	Thr	Thr	Asp	His	Leu	Ser	Pro	Ser	Asn	Ala	Ile	Leu	Ala				
																645	650	655	
gtc	agt	gcc	gca	ggc	gag	tat	ttg	gcg	aaa	atg	ggc	ttg	cct	gaa	gaa	2016			
Val	Ser	Ala	Ala	Gly	Glu	Tyr	Leu	Ala	Lys	Met	Gly	Leu	Pro	Glu	Glu				
																660	665	670	
gac	ttc	aac	tct	tac	gca	acc	cac	cgc	ggc	gac	cac	ttg	acc	gcc	caa	2064			
Asp	Phe	Asn	Ser	Tyr	Ala	Thr	His	Arg	Gly	Asp	His	Leu	Thr	Ala	Gln				
																675	680	685	
cgc	gct	acc	ttc	gcc	aat	ccg	aaa	ctg	ttt	aac	gaa	atg	gtg	aaa	aac	2112			
Arg	Ala	Thr	Phe	Ala	Asn	Pro	Lys	Leu	Phe	Asn	Glu	Met	Val	Lys	Asn				
																690	695	700	
gaa	gac	ggc	agc	gtg	cgc	caa	ggc	tgc	ttc	gcc	cgc	gtc	gaa	ccc	gaa	2160			
Glu	Asp	Gly	Ser	Val	Arg	Gln	Gly	Ser	Phe	Ala	Arg	Val	Glu	Pro	Glu				
																705	710	715	720
ggc	gaa	acc	atg	cgc	atg	tgg	gaa	gcc	atc	gaa	acc	tat	atg	aac	cgc	2208			
Gly	Glu	Thr	Met	Arg	Met	Trp	Glu	Ala	Ile	Glu	Thr	Tyr	Met	Asn	Arg				
																725	730	735	
aaa	cag	ccg	ctc	atc	atc	att	gcc	ggt	gcg	gac	tat	ggt	caa	ggc	tca	2256			
Lys	Gln	Pro	Leu	Ile	Ile	Ile	Ala	Gly	Ala	Asp	Tyr	Gly	Gln	Gly	Ser				
																740	745	750	
agc	cgc	gac	tgg	gct	gca	aaa	ggc	gta	cgc	ctc	gcc	ggc	gta	gaa	gcg	2304			
Ser	Arg	Asp	Trp	Ala	Ala	Lys	Gly	Val	Arg	Leu	Ala	Gly	Val	Glu	Ala				
																755	760	765	
att	gtt	gcc	gaa	ggc	ttc	gag	cgt	atc	cac	cgc	acc	aac	ctt	atc	ggc	2352			
Ile	Val	Ala	Glu	Gly	Phe	Glu	Arg	Ile	His	Arg	Thr	Asn	Leu	Ile	Gly				
																770	775	780	
atg	ggc	gtg	ttg	ccg	ctg	cag	ttc	aaa	ccc	gac	acc	aac	cgc	cat	acc	2400			
Met	Gly	Val	Leu	Pro	Leu	Gln	Phe	Lys	Pro	Asp	Thr	Asn	Arg	His	Thr				
																785	790	795	800
ctg	caa	ctg	gac	ggc	acg	gaa	acc	tac	gac	gtg	gtc	ggc	gaa	cgc	aca	2448			

Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr
805 810 815
cgc cgc tgc gac ctg acc ctc gtg att cac cgt aaa aac ggc gaa acc 2496
Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr
820 825 830
gtc gaa gtt ccc gtt acc tgc cgc ctc gat act gca gaa gaa gta ttg 2544
Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu
835 840 845
gta tat gaa gcc ggc ggc gtg ttg caa cgg ttt gca cag gat ttt ttg 2592
Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu
850 855 860
gaa ggg aac gcg gct tag 2610
Glu Gly Asn Ala Ala
865

<210> 42
<211> 869
<212> PRT
<213> Neisseria meningitidis

<400> 42
Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu
1 5 10 15
Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser
20 25 30
Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
35 40 45
Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
50 55 60
Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
65 70 75 80
Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu
85 90 95
Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
100 105 110
Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp His Ser Leu
115 120 125
Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg
130 135 140
Gln Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp
145 150 155 160
Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly
165 170 175
Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val

09830433 081604

180	185	190
Lys Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His 195	200	205
Thr Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly 210	215	220
Leu Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu 225	230	235 240
Pro Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Gln Ala Gly Ile 245	250	255
Thr Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu 260	265	270
Arg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser 275	280	285
Leu Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe 290	295	300
Gly Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr 305	310	315 320
Leu Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr 325	330	335
Tyr Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val 340	345	350
Tyr Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met 355	360	365
Ala Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala 370	375	380
Ser Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met 385	390	395 400
Pro Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr 405	410	415
Ser Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala 420	425	430
Asn Cys Phe Gly Leu Lys Arg Lys Pro Trp Val Lys Thr Ser Phe Ala 435	440	445
Pro Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Gly Leu Leu 450	455	460
Pro Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr 465	470	475 480
Thr Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu 485	490	495
Ile Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg		

09830433-061601

500	505	510
Asn Phe Asp Gly Arg Val His	Pro Tyr Ala Lys Gln Ala Phe Leu Ala	
515	520	525
Ser Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe		
530	535	540
Asp Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg		
545	550	555
Leu Lys Asp Ile Trp Pro Ala Asp Glu Glu Ile Asp Ala Val Val Ala		
565	570	575
Glu Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Val Pro Met Phe		
580	585	590
Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg		
595	600	605
Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu		
610	615	620
Ala Gly Glu Arg Thr Leu Arg Gly Met Arg Pro Leu Ala Ile Leu Pro		
625	630	635
Asp Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala		
645	650	655
Val Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu		
660	665	670
Asp Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln		
675	680	685
Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn		
690	695	700
Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu		
705	710	715
Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg		
725	730	735
Lys Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser		
740	745	750
Ser Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala		
755	760	765
Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly		
770	775	780
Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr		
785	790	795
Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr		
805	810	815
Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr		

09030433-081604

830

Glu Gly Asn Ala Ala
865

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<210> 43
<211> 1170
<212> DNA
<213> Neisseria meningitidis
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<220>
<221> CDS
<222> (1) .. (1167)
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<210>	44
<211>	389
<212>	PRT

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<400> 44
Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser
  1          5          10          15

Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
          20          25          30

Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
          35          40          45

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
  50          55          60

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp
  65          70          75          80

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
          85          90          95

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
          100          105          110

Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro
          115          120          125

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala
  130          135          140

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu
  145          150          155          160

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu
          165          170          175

Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val
          180          185          190

Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile
          195          200          205

Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr
  210          215          220

Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu
  225          230          235          240

Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu
          245          250          255

Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val
          260          265          270

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Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr
 275 280 285

Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly
 290 295 300

Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
 305 310 315 320

Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly
 325 330 335

Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
 340 345 350

Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
 355 360 365

Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val
 370 375 380

Pro Glu Asp Cys Phe
 385

<210> 45
 <211> 954
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1) .. (951)

<400> 45
 atg cgc acg ccc ttt tgt tgg gca tac gcc aat gcc gcc cga ata tcg 48
 Met Arg Thr Pro Phe Cys Trp Ala Tyr Ala Asn Ala Ala Arg Ile Ser
 1 5 10 15

gca atg ctg ccc gcc tgt tgg gcc cag gcc atg ttg gcc gaa gta atc 96
 Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile
 20 25 30

agc tgc aac aag gct tcg tcg ctg ccg cag cct tcg gcc aga tcg gcc 144
 Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala
 35 40 45

ttt aaa tca acc tgc ttc atg ggt gat tct ccg tat ttg gtt cag ata 192
 Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile
 50 55 60

gac ttg gtt ttt gcc ccc cag gcc ggt gcc ttc ttt caa gcc gat tat 240
 Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr
 65 70 75 80

ttt gaa ttt gac ttt gct gcc gaa gcc cac ctg tgc cag cct gcc caa 288
 Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln
 85 90 95

090433-0860

atc ggc ggc ggc aac ggt agc gat ttt cgg ata acc gcc ggt ggt ttg Ile Gly Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu	336
100 105 110	
cgc atc ggc cag cag gat aat cgg ttt gcc gcc ggg cgg cac ctg cac Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His	384
115 120 125	
ggt tcc tgc ctg aac agc gtg gga cag cat ttc caa agg ttg cga cag Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln	432
130 135 140	
ggt cag cgg ctg tcc gtc gaa gcg gta gcc cat gcg gtt gct atc gct Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala	480
145 150 155 160	
ttg cag cgt cca cgt ttc ccg ttc cag att cag acg ccc ttt ttc act Leu Gln Arg Pro Arg Phe Pro Phe Gln Ile Gln Thr Pro Phe Phe Thr	528
165 170 175	
gaa agc ggc ata ttc cga cga agg aac aag gtg gat ggt atc ggt aaa Glu Ser Gly Ile Phe Arg Arg Arg Asn Lys Val Asp Gly Ile Gly Lys	576
180 185 190	
cgg tat cgg ggc aat gcc gac ttt gga caa ttc ctg cgc acc ttt gcc Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Thr Phe Ala	624
195 200 205	
gat ggg gag ata atc gcc ttt ttg cag cat tct gcc ctg atg gcc gcc Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala	672
210 215 220	
gaa acc ggc ttt cag gtc ggt got tct cga acc cat cac ttc cgg cac Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His	720
225 230 235 240	
atc aaa tcc gcc cgc cac gca cac ata gcc gta cat gcc ctg cac ggc Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly	768
245 250 255	
acg cac cat ttt caa ggt ctg ccc ttt gcg ggc ggt ata acg cca ata Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile	816
260 265 270	
cga ata gac cgg ttc gcc gtc caa ttc cgc ctg ata cac ggc acc ggt Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly	864
275 280 285	
gag aca aaa cgg cgt atc ccg ttc aaa cac cag cat tat ccc gcc caa Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln	912
290 295 300	
agc gat ttc gat tgc gcc cgt gcc ttc gtc gtt gcc caa taa Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln	954
305 310 315	

<210> 46
 <211> 317
 <212> PRT
 <213> Neisseria meningitidis

109780-EE40E350

<400> 46

Met Arg Thr Pro Phe Cys Trp Ala Tyr Ala Asn Ala Ala Arg Ile Ser
 1 5 10 15

Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile
 20 25 30

Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala
 35 40 45

Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile
 50 55 60

Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr
 65 70 75 80

Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln
 85 90 95

Ile Gly Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu
 100 105 110

Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His
 115 120 125

Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln
 130 135 140

Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala
 145 150 155 160

Leu Gln Arg Pro Arg Phe Pro Phe Gln Ile Gln Thr Pro Phe Phe Thr
 165 170 175

Glu Ser Gly Ile Phe Arg Arg Arg Asn Lys Val Asp Gly Ile Gly Lys
 180 185 190

Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Thr Phe Ala
 195 200 205

Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala
 210 215 220

Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His
 225 230 235 240

Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly
 245 250 255

Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile
 260 265 270

Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly
 275 280 285

Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln
 290 295 300

Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln
 305 310 315

<210> 47

001601-00000000

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<220>  
<221> CDS  
<222> (1) .. (645)
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<400> 47																	
atg	aga	ata	gag	atc	aca	cca	atc	agc	gaa	tcc	gct	ttg	gtc	tgc	cga	48	
Met	Arg	Ile	Glu	Ile	Thr	Pro	Ile	Ser	Glu	Ser	Ala	Leu	Val	Cys	Arg		
1				5					10					15			
ctg	aat	gcg	cct	tcc	gaa	ctg	ggc	aaa	cag	caa	aag	ttg	tgg	gcg	ttt	96	
Leu	Asn	Ala	Pro	Ser	Glu	Leu	Gly	Lys	Gln	Gln	Lys	Leu	Trp	Ala	Phe		
			20					25					30				
gcc	gct	gcg	ctc	ggg	cag	cac	gac	agg	att	gag	gaa	gtg	gtg	gtc	ggc	144	
Ala	Ala	Ala	Leu	Gly	Gln	His	Asp	Arg	Ile	Glu	Glu	Val	Val	Val	Gly		
			35				40					45					
atg	aac	aat	ctg	acc	gtg	ttc	acc	cgt	ttc	gat	acc	gat	ttg	gcg	acg	192	
Met	Asn	Asn	Leu	Thr	Val	Phe	Thr	Arg	Phe	Asp	Thr	Asp	Leu	Ala	Thr		
	50					55					60						
ctt	gcc	gat	gaa	ttg	caa	tat	gtg	tgg	gaa	cac	acc	gcc	ggt	aca	gac	240	
Leu	Ala	Asp	Glu	Leu	Gln	Tyr	Val	Trp	Glu	His	Thr	Ala	Val	Thr	Asp		
65					70					75					80		
cat	cag	ggc	aaa	ctg	gtg	gaa	att	ccc	gtc	tgc	tac	ggc	ggc	gaa	tac	288	
His	Gln	Gly	Lys	Leu	Val	Glu	Ile	Pro	Val	Cys	Tyr	Gly	Gly	Glu	Tyr		
				85					90					95			
ggc	cgc	gat	ttg	gcg	gaa	gtc	gct	gct	ttc	cat	cag	acg	gtc	att	tcc	336	
Gly	Pro	Asp	Leu	Ala	Glu	Val	Ala	Ala	Phe	His	Gln	Thr	Val	Ile	Ser		
			100					105					110				
gaa	atc	gtc	cgc	cgc	cat	acg	ggc	caa	act	tat	acc	gta	ttt	atg	atg	384	
Glu	Ile	Val	Arg	Arg	His	Thr	Ala	Gln	Thr	Tyr	Thr	Val	Phe	Met	Met		
			115				120					125					
ggc	ttc	cag	cct	ggt	ttc	cct	tat	ctg	ggc	ggc	ttg	ccc	gaa	gca	ttg	432	
Gly	Phe	Gln	Pro	Gly	Phe	Pro	Tyr	Leu	Gly	Gly	Leu	Pro	Glu	Ala	Leu		
	130					135					140						
cac	acg	ccc	cgc	cgt	gcc	gtg	cgc	aga	acg	tcc	gtt	cct	gcc	ggt	tgc	480	
His	Thr	Pro	Arg	Arg	Ala	Val	Pro	Arg	Thr	Ser	Val	Pro	Ala	Gly	Ser		
145					150					155					160		
gtc	ggt	atc	ggc	ggc	agt	cag	acc	ggt	gtg	tat	ccg	ttc	gct	tgc	ccc	528	
Val	Gly	Ile	Gly	Gly	Ser	Gln	Thr	Gly	Val	Tyr	Pro	Phe	Ala	Ser	Pro		
				165					170					175			

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ggc ggc tgg cag att atc ggc aga acc gaa tta ccc ttg ttc cga gcc 576
Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala
      180                      185                      190

gat ttg aat ccg ccg acc ctg ctg gcg gcg ggt gac caa gtc cgc ttt 624
Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe
      195                      200                      205

gtt gca gaa agg att gag cca tga 648
Val Ala Glu Arg Ile Glu Pro
      210                      215

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<210> 48
 <211> 215
 <212> PRT
 <213> Neisseria meningitidis

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<400> 48
Met Arg Ile Glu Ile Thr Pro Ile Ser Glu Ser Ala Leu Val Cys Arg
  1                      5                      10                      15

Leu Asn Ala Pro Ser Glu Leu Gly Lys Gln Gln Lys Leu Trp Ala Phe
      20                      25                      30

Ala Ala Ala Leu Gly Gln His Asp Arg Ile Glu Glu Val Val Val Gly
      35                      40                      45

Met Asn Asn Leu Thr Val Phe Thr Arg Phe Asp Thr Asp Leu Ala Thr
      50                      55                      60

Leu Ala Asp Glu Leu Gln Tyr Val Trp Glu His Thr Ala Val Thr Asp
      65                      70                      75                      80

His Gln Gly Lys Leu Val Glu Ile Pro Val Cys Tyr Gly Gly Glu Tyr
      85                      90                      95

Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser
      100                      105                      110

Glu Ile Val Arg Arg His Thr Ala Gln Thr Tyr Thr Val Phe Met Met
      115                      120                      125

Gly Phe Gln Pro Gly Phe Pro Tyr Leu Gly Gly Leu Pro Glu Ala Leu
      130                      135                      140

His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser
      145                      150                      155                      160

Val Gly Ile Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro
      165                      170                      175

Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala
      180                      185                      190

Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe
      195                      200                      205

Val Ala Glu Arg Ile Glu Pro
      210                      215

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09630433-084604

<210> 49
 <211> 930
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1) .. (927)

<400> 49
 atg att cac gtt tgc gca gtg cag gca ccg gcg cat att cag gat acc 48
 Met Ile His Val Ser Ala Val Gln Ala Pro Ala His Ile Gln Asp Thr
 1 5 10 15
 gga cgc tac gga cac cgg cgt tac ggc atc ggt cat gcc ggt gcg atg 96
 Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met
 20 25 30
 gac acg gtt gct ttg gcg gcg ggt aat att tta ttg ggc aac gac gaa 144
 Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu
 35 40 45
 ggc acg gcc gca atc gaa atc gct ttg ggc ggg ata atg ctg gtg ttt 192
 Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
 50 55 60
 gaa cgs gat acg ccg ttt tgt ctc acc ggt gcc gcg tat cag gcc gaa 240
 Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu
 65 70 75 80
 ttg gac gcc gaa ccg gtc tat tgc tat tgg cgt tat acc gcc cgc aaa 288
 Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys
 85 90 95
 ggg cag acc ttg aaa atg gtg cgt gcc gtg cag gcc atg tac gcc tat 336
 Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr
 100 105 110
 gtg tgc gtg gcg gcc gga ttt gat gtg ccg gaa gtg atg ggt tgc aga 384
 Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg
 115 120 125
 agc acc gac ctg aaa gcc ggt ttc gcc gcc cat cag gcc aga atg ctg 432
 Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu
 130 135 140
 caa aaa gcc gat tat ctc ccc atc gcc aaa ggt gcg cag gaa ttg tcc 480
 Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser
 145 150 155 160
 aaa gtc gcc att gcc ccg ata ccg ttt acc gat acc atc cac ctt gtt 528
 Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val
 165 170 175
 cct tgc tgc gaa tat gcc gct ttc agt gaa aaa ggg cgt ctg aat ctg 576
 Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu
 180 185 190

0980433 081601

gaa cgg gaa acg tgg acg ctg caa agc gat agc aac cgc atg ggc tac 624
 Glu Arg Glu Thr Trp Thr Leu Gln Ser Asp Ser Asn Arg Met Gly Tyr
 195 200 205

cgc ttc gac gga cag ccg ctg acc ctg tgg caa cct ttg gaa atg ctg 672
 Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu
 210 215 220

tcc cac gct gtt cag gca gga acc gtg cag gtg cgc ccc ggc ggc aaa 720
 Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys
 225 230 235 240

ccg att atc ctg ctg gcc gat gcg caa acc acc ggc ggt tat ccg aaa 768
 Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys
 245 250 255

atc gct acc gtt gcc gcc gcc gat ttg ggc agg ctg gca cag gtg cgc 816
 Ile Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg
 260 265 270

ttc ggc agc aaa gtc aaa ttc aaa ata atc ggc ttg aaa gaa gcc acc 864
 Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr
 275 280 285

gcc ctg cgg cgc aaa aac caa gtc tat ctg aac caa ata cgg aga atc 912
 Ala Leu Arg Arg Lys Asn Gln Val Tyr Leu Asn Gln Ile Arg Arg Ile
 290 295 300

acc cat gaa gca ggt tga 930
 Thr His Glu Ala Gly
 305

<210> 50
 <211> 309
 <212> PRT
 <213> Neisseria meningitidis

<400> 50
 Met Ile His Val Ser Ala Val Gln Ala Pro Ala His Ile Gln Asp Thr
 1 5 10 15

Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met
 20 25 30

Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu
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Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
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Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu
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Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr
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Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg
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Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu
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Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser
 145 150 155 160

Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val
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Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu
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Glu Arg Glu Thr Trp Thr Leu Gln Ser Asp Ser Asn Arg Met Gly Tyr
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Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu
 210 215 220

Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys
 225 230 235 240

Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys
 245 250 255

Ile Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg
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Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr
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 Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
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att tct gta ttt atg gtc ggc ttg ggt gta ggt gcg tat ttc ggt gga	192
Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly	
50 55 60	
cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc	240
Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile	
65 70 75 80	
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Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Arg Gly Leu Ile	
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tcc gcc ttg ggg cag ctc tta gtt gag gct gat ttg ccc atc atc gct	336
Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala	
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Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala	
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acc ttg ccc ttg ctg acc tgt ttt ttt aac cgg aaa ata cat aat gct	432
Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val	
130 135 140	
ggc gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt gcg gca	480
Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala	
145 150 155 160	
ccc gga tcc ctt gcc gcc gct gaa ttt ttt ttc gtc ttt ttt acc ctc	528
Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu	
165 170 175	
tcc caa acc att gcc ctg aca gcc tgc ttt aac ctt ctg att gct gct	576
Ser Glu Thr Ile Ala Leu Thr Ala Cys Phe Asn Leu Leu Ile Ala Ala	
180 185 190	
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Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro	
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Asn Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser	
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225 230 235 240	
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Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly	
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atc gcc gtc ggc gcc tat ttt gcc aaa cgg att tgc cgc agc cgc ttt	816
Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe	
260 265 270	

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gtt gat att ccc ttt atc ggg cag tgc ttc ttg ttg ggc ggt att gcc	864
Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala	
275 280 285	
gac ttt ttg att ttg ggt gct gcg tgg ttg ttg acg ggt ttt tcc gcc	912
Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly	
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Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg	
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Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys	
325 330 335	
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Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser	
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gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttc ttg tcc	1104
Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser	
355 360 365	
acc caa cag att tac ctg ctg atc tgt ttg att tct gct gct gtc cct	1152
Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro	
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Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser	
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Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp	
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Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn	
420 425 430	
aaa cac ggc att gct gcg gtt tac cat aga gat ggt gat aag gtt gtt	1344
Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val	
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Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn	
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Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser	
465 470 475 480	
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Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala	
485 490 495	
cgc gtc ttg tct gcc att ccg gaa atg cag tgg atg atc gtt gcg gaa	1536
Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu	
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ccg	ctt	ttg	cag	gac	aaa	cgt	gtt	gaa	att	gta	ttg	gat	gac	ggc	agg	1632
Pro	Leu	Leu	Gln	Asp	Lys	Arg	Val	Glu	Ile	Val	Leu	Asp	Asp	Gly	Arg	
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aaa	tgg	ctg	cgt	cgc	cat	ccg	gat	gaa	aaa	ttc	gac	ctg	att	ttg	atg	1680
Lys	Trp	Leu	Arg	Arg	His	Pro	Asp	Glu	Lys	Phe	Asp	Leu	Ile	Leu	Met	
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aat	acg	act	tgg	tac	tgg	cgt	gcc	tat	tcc	acc	aac	ctg	ttg	agt	gcg	1728
Asn	Thr	Thr	Trp	Tyr	Trp	Arg	Ala	Tyr	Ser	Thr	Asn	Leu	Leu	Ser	Ala	
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gaa	ttt	tta	aaa	cag	gtg	caa	agc	cat	ctt	acc	ccg	gat	ggc	att	gta	1776
Glu	Phe	Leu	Lys	Gln	Val	Gln	Ser	His	Leu	Thr	Pro	Asp	Gly	Ile	Val	
			580					585					590			
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Met	Phe	Asn	Thr	Thr	His	Ser	Pro	His	Ala	Phe	Ala	Thr	Ala	Val	His	
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agt	att	ccc	tat	gca	tac	cgc	tat	ggg	cat	atg	gta	gtc	ggc	tgc	gca	1872
Ser	Ile	Pro	Tyr	Ala	Tyr	Arg	Tyr	Gly	His	Met	Val	Val	Gly	Ser	Ala	
		610				615					620					
acc	ccg	gta	gct	ttc	ccc	aat	aaa	gaa	ctg	ccc	aag	caa	cgt	ctc	tcc	1920
Thr	Pro	Val	Val	Phe	Pro	Asn	Lys	Glu	Leu	Leu	Lys	Gln	Arg	Leu	Ser	
		625				630				635					640	
agg	ttg	att	tgg	ccg	gaa	agc	ggc	agg	cac	gta	ttt	gac	agc	agc	acc	1968
Arg	Leu	Ile	Trp	Pro	Glu	Ser	Gly	Arg	His	Val	Phe	Asp	Ser	Ser	Thr	
				645				650					655			
gtg	gat	gct	gca	gca	caa	aag	gct	gtc	tcc	cgt	atg	ctg	att	cag	atg	2016
Val	Asp	Ala	Ala	Ala	Gln	Lys	Val	Val	Ser	Arg	Met	Leu	Ile	Gln	Met	
			660					665					670			
acg	gaa	ccc	tgc	gct	ggg	gcg	gaa	gtc	att	acc	gac	gat	aat	atg	att	2064
Thr	Glu	Pro	Ser	Ala	Gly	Ala	Glu	Val	Ile	Thr	Asp	Asp	Asn	Met	Ile	
		675				680						685				
gta	gaa	tac	aaa	tac	ggc	aga	ggg	att	taa							2094
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Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
 35 40 45
 Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
 50 55 60
 Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile
 65 70 75 80
 Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Arg Gly Leu Ile
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 Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala
 100 105 110
 Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala
 115 120 125
 Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val
 130 135 140
 Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala
 145 150 155 160
 Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu
 165 170 175
 Ser Gln Thr Ile Ala Leu Thr Ala Cys Phe Asn Leu Leu Ile Ala Ala
 180 185 190
 Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro
 195 200 205
 Asn Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser
 210 215 220
 Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln
 225 230 235 240
 Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly
 245 250 255
 Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe
 260 265 270
 Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala
 275 280 285
 Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly
 290 295 300
 Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg
 305 310 315 320
 Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys
 325 330 335
 Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser
 340 345 350

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Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser
355 360 365

Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro
370 375 380

Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser
385 390 395 400

Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp
405 410 415

Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn
420 425 430

Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val
435 440 445

Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn
450 455 460

Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser
465 470 475 480

Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala
485 490 495

Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu
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Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala
515 520 525

Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg
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Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met
545 550 555 560

Asn Thr Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala
565 570 575

Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val
580 585 590

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His
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Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala
610 615 620

Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser
625 630 635 640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
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Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Gln Met
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Ala Val Ser Tyr Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser
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Met Leu Cys Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala
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Lys Ile Asn Ala Pro Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn
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Pro Asn Asp Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu
85 90 95

Ala Gly Tyr Thr Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly
100 105 110

Glu Ser Val Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu
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His Gly Tyr Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys
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Glu Ala Pro Glu Asp Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp
145 150 155 160

Asp Glu Ala Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His
165 170 175

Val Lys Glu Ile Gly His Ile Asp Val Val Ser His Ile Ile Gly Gly
180 185 190

Arg Ser Val Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr
195 200 205

Leu His Ile Met Asn Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser
210 215 220

Ala Ala Ile Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg
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Ile Val Asn Asn Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp
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His Phe Gln Ile Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu
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Ala Tyr Ser Gly Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln
275 280 285

Gln Ser Asp Tyr Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met
290 295 300

Leu Phe Ile Phe Ser Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr
305 310 315 320

Leu Thr Leu Leu Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile
325 330 335

Thr Val Ala Gly Val Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn
340 345 350

His Cys Gly Ile Thr Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala
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Ser Val Arg Phe Thr Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser
370 375 380

Phe Ser Ala Pro Ile Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys
385 390 395 400

Tyr Pro Trp Met Ser Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr
405 410 415

Ala Gln Asp Ile Gly Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly
420 425 430

Leu Leu Asp Ala Gly Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe
435 440 445

Gly Asp Phe Thr Ala Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser
450 455 460

Phe Arg Asn Asp Ile Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly
465 470 475 480

Ser Gln Leu Gln Leu His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile
485 490 495

Ile Glu Gly Gly Ser Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met
500 505 510

Arg Val Glu Thr Lys Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly
515 520 525

Gly Ser Leu Asn Ser Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg
530 535 540

Ser Gly Ala Asn Glu Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly
545 550 555 560

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Gly Glu Gly Thr Leu Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp
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Gly Thr Ala Met Thr Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys
580 585 590

Gly Ala Gly Tyr Leu Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser
595 600 605

Ala Ala Lys Ile Gly Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr
610 615 620

Asp Gly Gly Leu Leu Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly
625 630 635 640

Ser Glu Gly Asp Thr Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala
645 650 655

Arg Thr Ala Ser Ala Ala Ala His Ser Ala Pro Ala Gly Leu Lys His
660 665 670

Ala Val Glu Gln Gly Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu
675 680 685

Asp Ala Ser Glu Ser Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala
690 695 700

Ala Asp Arg Thr Asp Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe
705 710 715 720

Arg Ala Ala Ala Ala Val Gln His Ala Asn Ala Ala Asp Gly Val Arg
725 730 735

Ile Phe Asn Ser Leu Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala
740 745 750

His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu
755 760 765

Asp His Asn Ala Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp
770 775 780

Gly Gly Thr Trp Glu Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser
785 790 795 800

Thr Gln Thr Val Gly Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala
805 810 815

Ala Ala Thr Leu Gly Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala
820 825 830

Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp
835 840 845

Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr
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1				5					10					15		
cat	ttg	ggt	gta	aag	atg	tat	tcg	cac	act	gtt	cct	gcg	att	gcc	gag	96
His	Leu	Gly	Val	Lys	Met	Tyr	Ser	His	Thr	Val	Pro	Ala	Ile	Ala	Glu	
			20					25					30			
ttg	ata	gcg	aat	gcc	tac	gat	gca	tgt	gct	acg	gaa	gtg	gaa	gtt	agg	144
Leu	Ile	Ala	Asn	Ala	Tyr	Asp	Ala	Cys	Ala	Thr	Glu	Val	Glu	Val	Arg	
		35					40					45				
tta	ttc	gat	aaa	ccg	gag	cat	aaa	atc	gtt	att	aaa	gat	aat	ggc	ata	192
Leu	Phe	Asp	Lys	Pro	Glu	His	Lys	Ile	Val	Ile	Lys	Asp	Asn	Gly	Ile	
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Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg	
65 70 75 80	
aac aga agg gaa gaa aaa caa gcc tcc ccg tgc gga aga att cca acg	288
Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr	
85 90 95	
ggt aaa aaa ggt ctt ggt aaa ttg gca tta ttc agg ctt ggc aac aaa	336
Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys	
100 105 110	
atc gaa atc tct act atc caa gga aac gaa ccg gtt act ttt act ttg	384
Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu	
115 120 125	
gat tat gca gag att aaa aaa agt gag cgt att tat caa ccg gag ttt	432
Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe	
130 135 140	
cag aaa gag tct gtt aaa ccc aat acc gaa aac gga acc act ata act	480
Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr	
145 150 155 160	
tta acc gag ctg acg aaa aaa caa gga tac ccg tta gat aat tat gtg	528
Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val	
165 170 175	
ggg cat ctt tcc cgt tta ttt gat ttt ccg gct cag gat ttt aaa atc	576
Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile	
180 185 190	
aaa gta agc ttg aac ggc tgc gaa cca aga atc att gac gga aac cta	624
Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu	
195 200 205	
aaa tat aat ctt gtt acc cca caa ttc gaa tgg gaa tac cag gat cta	672
Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu	
210 215 220	
gca acc aat att tca tgc tta tct tca aaa ttc gaa cag tat gaa tac	720
Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr	
225 230 235 240	
agc gga tta ata caa ggt aag ttc att aca acg gaa aaa cct tta aag	768
Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys	
245 250 255	
aat aat atg aaa ggt att acc ttg ttt gcc aac ggc aga atg gta aat	816
Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn	
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Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe	
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His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu
20 25 30

Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg
35 40 45

Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile
50 55 60

Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg
65 70 75 80

Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr
85 90 95

Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys
100 105 110

Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu
115 120 125

Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe
130 135 140

Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr
145 150 155 160

Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val
165 170 175

Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile
180 185 190

Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu
195 200 205

Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu
210 215 220

Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr
225 230 235 240

Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys
245 250 255

Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn
260 265 270

Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe
275 280 285

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0930133-081604

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1 5 10 15	
gcc agc gaa atc gcc tat cgc ttt gta ttc gga att gaa acc tta ccg	96
Ala Ser Glu Ile Ala Tyr Arg Phe Val Phe Gly Ile Glu Thr Leu Pro	
20 25 30	
gct gca aaa atg gcg gaa acg ttt gcg ctg aca ttt atg att gct gcg	144
Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala	
35 40 45	
ctg tat ctg ttc gcg cgt tat aag gct tcg cgg ctg ctg att gcg gtg	192
Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val	
50 55 60	
ttt ttc gcg ttc agc atg att gcc aac aat gtg cat tac gcg gtt tat	240
Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr	
65 70 75 80	
caa agc tgg atg acg ggt att aac tat tgg ctg atg ctg aaa gag gtt	288
Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val	
85 90 95	
acc gaa gtc ggc agc gcg ggc gcg tcg atg ttg gat aag ttg tgg ctg	336
Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu	
100 105 110	
cct gct ttg tgg ggc gtg gcg gaa gtc atg ttg ttt tgc agc ctt gcc	384
Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala	
115 120 125	
aag ttc cgc cgt aag acg cat ttt tct gcc gat ata ctg ttt gcc ttc	432
Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe	
130 135 140	
cta atg ctg atg att ttc gtg cgt tcg ttc gac acg aaa caa gag cac	480
Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His	
145 150 155 160	
ggt att tcg ccc aaa ccg aca tac agc cgc atc aaa gcc aat tat ttc	528
Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe	
165 170 175	
agc ttc ggt tat ttt gtc ggg cgc gtg ttg ccg tat cag ttg ttt gat	576
Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp	
180 185 190	
tta agc aag atc cct gtg ttc aaa cag cct gct cca agc aaa atc ggg	624
Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly	

05830433 084604

195				200				205								
caa Gln 210	ggc Ser	agt Ile	att Ile	caa Gln	aat Asn	atc Ile 215	gtc Val	ctg Leu	att Ile	atg Met	ggc Gly 220	gaa Glu	agc Ser	gaa Glu	agc Ser	672
gcg Ala 225	gcg Ala	cat His	ttg Leu	aaa Lys 230	ttg Leu 230	ttt Phe 230	ggg Gly	tac Tyr	ggg Gly 235	ggc Arg 235	gaa Glu	act Thr	tcg Ser	ccg Pro	ttt Phe 240	720
tta Leu	acc Thr	cgg Arg	ctg Leu 245	tcg Ser 245	caa Gln	gcc Ala	gat Asp	ttt Phe 250	aag Lys 250	ccg Pro	att Ile	gtg Val	aaa Lys 255	caa Gln 255	agt Ser	768
tat Tyr	tcc Ser	gca Ala 260	ggc Gly 260	ttt Phe	atg Met	acg Thr	gca Ala 265	gta Val 265	tcc Ser	ctg Leu	ccc Pro	agt Ser 270	ttc Phe 270	ttt Phe	aac Asn	816
gtc Val	ata Ile 275	ccg Pro	cac His	gcc Ala	aac Asn	ggc Gly 280	ttg Leu 280	gaa Glu	caa Gln	atc Ile	agc Ser	ggc Gly 285	ggc Gly	gat Asp	acc Thr	864
aat Asn 290	atg Met	ttc Phe	cgc Arg	ctc Leu	gcc Ala	aaa Lys 295	gag Glu	cag Gln	ggc Gly	tat Tyr	gaa Glu 300	acg Thr	tat Tyr	ttt Phe	tac Tyr	912
agt Ser 305	gcc Ala	cag Gln	gct Ala	gaa Glu	aac Asn 310	caa Gln	atg Met	gca Ala	att Ile	ttg Leu 315	aac Asn	tta Leu	atc Ile	ggg Gly	aag Lys 320	960
aaa Lys	tgg Trp	ata Ile	gac Asp	cat His 325	ctg Leu	att Ile	cag Gln	ccg Pro	acg Thr 330	caa Gln	ctt Leu	ggc Gly	tac Tyr	ggc Gly 335	aac Asn	1008
ggc Gly	gac Asp	aat Asn 340	atg Met	ccc Pro	gat Asp	gag Glu	aag Lys	ctg Leu 345	ctg Leu	ccg Pro	ttg Leu	ttc Phe	gac Asp 350	aaa Lys	atc Ile	1056
aat Asn 355	ttg Leu	cag Gln	cag Gln	ggc Gly	agg Arg	cat His	ttt Phe 360	atc Ile	gtg Val	ttg Leu	cac His	caa Gln 365	cgc Arg	ggg Gly	tcg Ser	1104
cac His 370	gcc Ala	cca Pro	tac Tyr	ggc Gly	gca Ala	ttg Leu 375	ttg Leu	cag Gln	cct Pro	caa Gln	gat Asp 380	aaa Lys	gta Val	ttc Phe	ggc Gly	1152
gaa Glu 385	gcc Ala	gat Asp	att Ile	gtg Val	gat Asp 390	aag Lys	tac Tyr	gac Asp	aac Asn	acc Thr 395	atc Ile	cac His	aaa Lys	acc Thr	gac Asp 400	1200
caa Gln	atg Met	att Ile	caa Gln	acc Thr 405	gta Val	ttc Phe	gag Glu	cag Gln	ctg Leu 410	caa Gln	aag Lys	cag Gln	cct Pro	gac Asp 415	ggc Gly	1248
aac Asn	tgg Trp	ctg Leu	ttt Phe 420	gcc Ala	tat Tyr	acc Thr	tcc Ser	gat Asp 425	cat His	ggc Gly	cag Gln	tat Tyr	gtg Val 430	cgc Arg	caa Gln	1296
gat Asp	atc Ile	tac Tyr	aat Asn	caa Gln	ggc Gly	acg Thr	gtg Val	cag Gln	ccc Pro	gac Asp	agc Ser	tat Tyr	att Ile	gtg Val	cct Pro	1344

435	440	445	
ctg gtt ttg tac agc ccg gat aag gcc gtg caa cag gct gcc aac cag			1392
Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln			
450	455	460	
gct ttt gcg cct tgc gag att gcc ttc cat cag cag ctt tca acg ttc			1440
Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe			
465	470	475	480
ctg att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa			1488
Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu			
	485	490	495
ggc tcg gta aca ggc aac ctg att acg gcc gat gca ggc agc ttg aac			1536
Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn			
	500	505	510
att cgc aac gcc aag gcg gaa tat gtt tat ccg caa taa			1575
Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln			
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 Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala
 35 40 45
 Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val
 50 55 60
 Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr
 65 70 75 80
 Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val
 85 90 95
 Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu
 100 105 110
 Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala
 115 120 125
 Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe
 130 135 140
 Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His
 145 150 155 160
 Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe

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	165		170		175
Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp	180		185		190
Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly	195		200		205
Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser	210		215		220
Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe	225		230		235
Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser	245		250		255
Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn	260		265		270
Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr	275		280		285
Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr	290		295		300
Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys	305		310		315
Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn	325		330		335
Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile	340		345		350
Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser	355		360		365
His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly	370		375		380
Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp	385		390		395
Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly	405		410		415
Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln	420		425		430
Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro	435		440		445
Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln	450		455		460
Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe	465		470		475
Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu					480

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485

490

495

Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn
500 505 510

Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln
515 520

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<211> 1314

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1) .. (1311)

<400> 58

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Met Leu Thr Phe Ile Gly Leu Leu Ile Ile Gly Val Ile Val Trp Leu
1 5 10 15

ttg ctg acg gaa aaa gtg tgg ccc atc atc gca tta atc ttg gtg ccg 96
Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro
20 25 30

ctg att ggg gcg ttg ctg ggc ggg ttt gat gta tcc caa tta aaa gaa 144
Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
35 40 45

ttt tat tgg ggc ggc acg aaa tgg gtg acg cag att gtg att atg ttt 192
Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe
50 55 60

atg ttt tcc att ttg ttt ttt gga atc atg aac gat gtg ggg ctg ttc 240
Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe
65 70 75 80

cgt ccg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg 288
Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val
85 90 95

gca gtg agt gtg ggg acg gtc ttg gtg tgg gtg gca cag ttg gac 336
Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
100 105 110

ggg gcg ggc ggc acg acg ttt tta tgg gtc gtc ccc gcc ctt ttg ccg 384
Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro
115 120 125

ctt tac aag cgt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg 432
Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
130 135 140

act tcc agc gcg ggg cta atc aac ctt ttg ccg cgg ggc ggg ccg atc 480
Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile
145 150 155 160

09830433-081601

ggg cgg gtt gca agc gtg ttg ggc gca gat gtg ggc gaa ttg tat aaa	528
Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys	
165 170 175	
cct ttg ttg acg gtg caa att atc ggt gtg gtg ttt atc ctt gtg ctg	576
Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Val Leu	
180 185 190	
tcc ctg ttt ttg ggt gtg cgt gaa aaa agg cgg att gtc cgg gag ttg	624
Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu	
195 200 205	
ggc gcg ttg ccc gcc gtg gcg gat ttg ata aag ccg gcg cct ttg tcg	672
Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser	
210 215 220	
gaa gaa gaa caa aaa ttg gcg cgt ccg aaa ctg ttt tgg tgg aat gtc	720
Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val	
225 230 235 240	
ctg ctg ttt ttg gcg gcg atg agc ctg ctt ttt tgg ggc atc ttc ccg	768
Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro	
245 250 255	
ccg ggt tat gta ttt atg ctg gct gca acg gcg gcg ttg ctt ttg aat	816
Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Asn	
260 265 270	
tac cgc agc ccg cag gaa cag atg gag cgg att tat gcc cac gcc ggc	864
Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly	
275 280 285	
ggc gcg gtg atg atg gcg tcc att att ttg gcg gca ggt acg ttt ttg	912
Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu	
290 295 300	
ggg att ttg aag ggc gcg ggg atg ttg gac gcg att tcc aaa gac ctt	960
Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu	
305 310 315 320	
gtg cat atc ctg ccg gac gcg ttg ctg cct tat ctg cat att gcc atc	1008
Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile	
325 330 335	
ggg gtg ttg ggt att ccg ctt gag ttg gtt ttg agt acg gac gct tat	1056
Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr	
340 345 350	
tat ttc gga ctg ttt ccg att gtg gaa cag att acc tgg cag gcg ggc	1104
Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly	
355 360 365	
gtt gca ccc gaa gcg gca ggc tat gcg atg ttg atc ggc agt atc gtc	1152
Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val	
370 375 380	
ggg act ttt gtt acg ccg ctt tgg ccg gct ttg tgg atg ggt ttg ggt	1200
Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly	
385 390 395 400	

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ttg gcg aaa ttg tgc atg ggc aaa cac atc cgt tat tgc ttt ttc tgg 1248
 Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
 405 410 415

gcg tgg ggt ttg tgc ctg gcg ata ttg gtc agt tgc ata gcg gca gga 1296
 Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly
 420 425 430

atc gtc cct ctg ccg taa 1314
 Ile Val Pro Leu Pro
 435

<210> 59
 <211> 437
 <212> PRT
 <213> Neisseria gonorrhoeae

<400> 59
 Met Leu Thr Phe Ile Gly Leu Leu Ile Ile Gly Val Ile Val Trp Leu
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Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro
 20 25 30

Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
 35 40 45

Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe
 50 55 60

Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe
 65 70 75 80

Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val
 85 90 95

Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
 100 105 110

Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro
 115 120 125

Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
 130 135 140

Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile
 145 150 155 160

Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys
 165 170 175

Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Val Leu
 180 185 190

Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu
 195 200 205

Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser
 210 215 220

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Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val
 225 230 235 240

Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro
 245 250 255

Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn
 260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
 275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu
 290 295 300

Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu
 305 310 315 320

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
 325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr
 340 345 350

Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly
 355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val
 370 375 380

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
 385 390 395 400

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
 405 410 415

Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly
 420 425 430

Ile Val Pro Leu Pro
 435

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 <211> 1155
 <212> DNA
 <213> Neisseria gonorrhoeae

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<400> 60
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 act tat ctg tat caa aag ccc aag ctc ttc aaa gga gcg gtt cgg aat 96

00330433 081601

Thr	Tyr	Leu	Tyr	Gln	Lys	Pro	Lys	Leu	Phe	Lys	Gly	Ala	Val	Arg	Asn	
			20					25					30			
ctc	gaa	gcc	gca	tct	tgt	aaa	tat	atc	aac	gag	ata	tac	caa	cga	gca	144
Leu	Glu	Ala	Ala	Ser	Cys	Lys	Tyr	Ile	Asn	Glu	Ile	Tyr	Gln	Arg	Ala	
		35					40					45				
gac	cca	acc	gca	ccg	ctg	ttt	cat	ctg	cgt	aaa	aaa	ggc	gca	atc	gtt	192
Asp	Pro	Thr	Ala	Pro	Leu	Phe	His	Leu	Arg	Lys	Lys	Gly	Ala	Ile	Val	
	50					55					60					
ccg	aaa	gaa	gaa	tac	gtc	gaa	agt	ttc	gac	gat	ttg	ggc	aaa	act	cgc	240
Pro	Lys	Glu	Glu	Tyr	Val	Glu	Ser	Phe	Asp	Asp	Leu	Gly	Lys	Thr	Arg	
	65				70				75						80	
tac	cgt	ttt	att	aaa	tcc	gtt	atc	tac	gaa	cat	atg	aag	aat	ggg	gcg	288
Tyr	Arg	Phe	Ile	Lys	Ser	Val	Ile	Tyr	Glu	His	Met	Lys	Asn	Gly	Ala	
				85				90						95		
tcg	tta	gtc	tat	aac	cat	att	aac	aac	gag	ccg	ttt	tca	gac	cat	atc	336
Ser	Leu	Val	Tyr	Asn	His	Ile	Asn	Asn	Glu	Pro	Phe	Ser	Asp	His	Ile	
			100					105					110			
gcc	cgt	caa	gtc	gcc	cgc	ttt	gcc	ggc	gca	cat	act	att	gtt	agt	gga	384
Ala	Arg	Gln	Val	Ala	Arg	Phe	Ala	Gly	Ala	His	Thr	Ile	Val	Ser	Gly	
		115					120					125				
tat	ctt	gct	ttt	ggc	agc	gac	gaa	tct	tat	aaa	aac	cat	tgg	gat	acc	432
Tyr	Leu	Ala	Phe	Gly	Ser	Asp	Glu	Ser	Tyr	Lys	Asn	His	Trp	Asp	Thr	
	130					135					140					
cgc	gat	gtg	tat	gcc	atc	cag	ctt	ttc	ggc	aag	aaa	cgt	tgg	caa	ctt	480
Arg	Asp	Val	Tyr	Ala	Ile	Gln	Leu	Phe	Gly	Lys	Lys	Arg	Trp	Gln	Leu	
	145				150					155					160	
act	gcc	cct	gat	ttc	cct	atg	cca	ttg	tat	atg	caa	cag	act	aaa	gat	528
Thr	Ala	Pro	Asp	Phe	Pro	Met	Pro	Leu	Tyr	Met	Gln	Gln	Thr	Lys	Asp	
				165				170					175			
act	gat	att	tcc	att	cct	gaa	cat	atc	gat	atg	gat	att	atc	ctt	gaa	576
Thr	Asp	Ile	Ser	Ile	Pro	Glu	His	Ile	Asp	Met	Asp	Ile	Ile	Leu	Glu	
			180					185					190			
gca	ggg	gat	gtc	ctc	tac	atc	cca	cgc	ggg	tgg	tgg	cac	aga	cct	atc	624
Ala	Gly	Asp	Val	Leu	Tyr	Ile	Pro	Arg	Gly	Trp	Trp	His	Arg	Pro	Ile	
		195					200					205				
ccg	ctc	ggc	tgt	gaa	acc	ttc	cac	ttc	gct	gtc	ggg	acc	ttc	cca	cca	672
Pro	Leu	Gly	Cys	Glu	Thr	Phe	His	Phe	Ala	Val	Gly	Thr	Phe	Pro	Pro	
	210					215					220					
aac	ggc	tat	aat	tac	ctc	gag	tgg	cta	atg	aag	aaa	ttt	ccc	acc	ata	720
Asn	Gly	Tyr	Asn	Tyr	Leu	Glu	Trp	Leu	Met	Lys	Lys	Phe	Pro	Thr	Ile	
	225				230				235						240	
gaa	agt	ctg	cgc	cac	agt	ttc	tca	gac	tgg	gag	caa	gat	agg	acg	cgt	768
Glu	Ser	Leu	Arg	His	Ser	Phe	Ser	Asp	Trp	Glu	Gln	Asp	Arg	Thr	Arg	
				245				250					255			
atc	aac	gat	act	gcc	gca	caa	att	gct	gcc	atg	att	gcc	gac	ccc	gtc	816

05030433-081604

Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val	
260 265 270	
aat tat gaa gcc ttc agt gaa gac ttt ctc ggc aaa gaa cgt acc gat	864
Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp	
275 280 285	
acc gct ttt cat ctc gaa cag ttc gcg aat ccc aac gct act ccg ctt	912
Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu	
290 295 300	
tca gac gac gtc agg ttg aga tta aat gcc aat aat ttg gat acg ttg	960
Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu	
305 310 315 320	
gaa aag gga tat ttg att ggg aat ggg atg aag ata agc gta gat gag	1008
Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu	
325 330 335	
ttg ggg aaa aaa gtg tta gaa cac atc ggt aag aat gaa ccg tta ttg	1056
Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu	
340 345 350	
ttg aaa aat cta ctg gtt aac ttc aat cag gca aaa cat gaa gaa gtt	1104
Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val	
355 360 365	
agg aag ttg atc tat cag ttg ata gag tta gat ttt ctg gaa att ttg	1152
Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Ile Leu	
370 375 380	
tga	1155

<210> 61
 <211> 384
 <212> PRT
 <213> Neisseria gonorrhoeae

<400> 61
 Met Gly Ile His Leu Asp Phe Gly Ile Ser Pro Lys Thr Phe Arg Gln
 1 5 10 15
 Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn
 20 25 30
 Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala
 35 40 45
 Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val
 50 55 60
 Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg
 65 70 75 80
 Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala
 85 90 95
 Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
 100 105 110

0030433-081601

Ala Arg Gln Val	Ala Arg Phe	Ala Gly Ala His Thr	Ile Val Ser Gly
115		120	125
Tyr Leu Ala Phe Gly Ser	Asp Glu Ser Tyr Lys	Asn His Trp Asp Thr	
130	135	140	
Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu			
145	150	155	160
Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp			
	165	170	175
Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu			
	180	185	190
Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile			
	195	200	205
Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro			
	210	215	220
Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile			
	225	230	235
Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg			
	245	250	255
Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val			
	260	265	270
Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp			
	275	280	285
Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu			
	290	295	300
Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu			
	305	310	315
Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu			
	325	330	335
Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu			
	340	345	350
Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val			
	355	360	365
Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Ile Leu			
	370	375	380

<210> 62
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 <212> DNA
 <213> Neisseria meningitidis
 <220>

00330433 081601

$\langle 222 \rangle \quad (1) \dots (714)$

atg	aat	aga	ccc	aag	caa	ccc	ttc	ttc	cgt	ccc	gaa	gtc	gcc	gtt	gcc	48
Met	Asn	Arg	Pro	Lys	Gln	Pro	Phe	Phe	Arg	Pro	Glu	Val	Ala	Val	Ala	
1				5					10					15		
cgc	caa	acc	agc	ctg	acg	ggg	aaa	gtg	att	ctg	aca	cga	ccg	ttg	tca	96
Arg	Gln	Thr	Ser	Leu	Thr	Gly	Lys	Val	Ile	Leu	Thr	Arg	Pro	Leu	Ser	
			20					25					30			
ttt	tcc	cta	tgg	acg	aca	ttt	gca	tcg	ata	tct	gcg	tta	ttg	att	atc	144
Phe	Ser	Leu	Trp	Thr	Thr	Phe	Ala	Ser	Ile	Ser	Ala	Leu	Leu	Ile	Ile	
		35					40					45				
ctg	ttt	ttg	ata	ttt	ggg	aac	tat	acg	cga	aag	aca	aca	gtg	gag	gga	192
Leu	Phe	Leu	Ile	Phe	Gly	Asn	Tyr	Thr	Arg	Lys	Thr	Thr	Val	Glu	Gly	
		50				55					60					
caa	att	tta	cct	gca	tcg	ggc	gta	atc	agg	gtg	tat	gca	ccg	gat	acg	240
Gln	Ile	Leu	Pro	Ala	Ser	Gly	Val	Ile	Arg	Val	Tyr	Ala	Pro	Asp	Thr	
65					70				75					80		
ggg	aca	att	aca	gcg	aaa	ttc	gtg	gaa	gat	gga	gaa	aag	gtt	aag	gct	288
Gly	Thr	Ile	Thr	Ala	Lys	Phe	Val	Glu	Asp	Gly	Glu	Lys	Val	Lys	Ala	
				85					90					95		
ggc	gac	aag	cta	ttt	gcg	ctt	tcg	acc	tca	cgt	ttc	ggc	gca	gga	gat	336
Gly	Asp	Lys	Leu	Phe	Ala	Leu	Ser	Thr	Ser	Arg	Phe	Gly	Ala	Gly	Asp	
			100					105					110			
agc	gtg	cag	cag	cag	ttg	aaa	acg	gag	gca	gtt	ttg	aag	aaa	acg	ttg	384
Ser	Val	Gln	Gln	Gln	Leu	Lys	Thr	Glu	Ala	Val	Leu	Lys	Lys	Thr	Leu	
		115					120					125				
gca	gaa	cag	gaa	ctg	ggg	cgt	ctg	aag	ctg	ata	cac	ggg	aat	gaa	acg	432
Ala	Glu	Gln	Glu	Leu	Gly	Arg	Leu	Lys	Leu	Ile	His	Gly	Asn	Glu	Thr	
		130				135					140					
cgc	agc	ctt	aaa	gca	act	gtc	gaa	cgt	ttg	gaa	aac	cag	gaa	ctc	cat	480
Arg	Ser	Leu	Lys	Ala	Thr	Val	Glu	Arg	Leu	Glu	Asn	Gln	Glu	Leu	His	
145					150					155					160	
att	tcg	caa	cag	ata	gac	ggg	cag	aaa	agg	cgc	att	aga	ctt	gcg	gaa	528
Ile	Ser	Gln	Gln	Ile	Asp	Gly	Gln	Lys	Arg	Arg	Ile	Arg	Leu	Ala	Glu	
				165					170					175		
gaa	atg	ttg	cag	aaa	tat	cgt	ttc	cta	tcc	gcc	aat	gat	gca	gtg	cca	576
Glu	Met	Leu	Gln	Lys	Tyr	Arg	Phe	Leu	Ser	Ala	Asn	Asp	Ala	Val	Pro	
			180					185					190			
aaa	caa	gaa	atg	atg	aat	gtc	aag	gca	gag	ctt	tta	gag	cag	aaa	gcc	624
Lys	Gln	Glu	Met	Met	Asn	Val	Lys	Ala	Glu	Leu	Leu	Glu	Gln	Lys	Ala	
		195					200					205				
aaa																

<210> 63

<213> Neisseria meningitidis

Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala
225 230 235

<213> Neisseria meningitidis

$\langle 220 \rangle$

<221> CDS

<222> (1)..(687)

<400> 64

atg atg aat gtc gag gca gag ctt tta gag cag aaa gcc aaa ctt gat	48
Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp	
1 5 10 15	
gcc tac ggc cga gaa gaa gcc ggg ctg ctt cag gaa atc cgc acg cag	96
Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln	
20 25 30	
aat ctg aca ttg gcc agc ctc ccc aaa cgg cat gag aca gaa caa agc	144
Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser	
35 40 45	
cag ctt gaa cgc acc atg gcc gat att tct caa gaa gtt ttg gat ttt	192
Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe	
50 55 60	
gaa atg cgc tct gaa caa atc atc cgt gca gga cgg tgg ggt tat ata	240
Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile	
65 70 75 80	
gca ata ccg aac gtc gaa gtc gga cgg cag gtt gat cct tcc aaa ctg	288
Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu	
85 90 95	
ctc ttg agc att gtt ccc gaa cgt acc gag tta tat gcc cat cta tat	336
Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr	
100 105 110	
atc ccc agc agt gca gca gcc ttt atc aag ccg aaa gac aag gtt gtc	384
Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val	
115 120 125	
cta cgt tat cag gca tat ccc tat cag aaa ttc ggg ctt gct tcc ggc	432
Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly	
130 135 140	
agt gtc gta tca gtg gca aaa acg gca ctg ggc aga cag gaa ttg tgg	480
Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser	
145 150 155 160	
gga ttg ggc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt	528
Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val	
165 170 175	
tat ctc gtg aaa ata aaa ccc gac aaa cca acc atc act gca tac ggt	576
Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly	
180 185 190	
gag gaa aaa ctg ctg caa atc gcc atg acg ctg gaa gca gac atc cta	624
Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu	
195 200 205	
cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag ccg att tac agt	672
His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser	
210 215 220	
atg tgg ggc agg ttg taa	690
Met Ser Gly Arg Leu	
225	

009180" E410E350

<210> 65
 <211> 229
 <212> PRT
 <213> Neisseria gonorrhoeae

<400> 65
 Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp
 1 5 10 15
 Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln
 20 25 30
 Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
 35 40 45
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
 50 55 60
 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
 65 70 75 80
 Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu
 85 90 95
 Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
 100 105 110
 Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
 115 120 125
 Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
 130 135 140
 Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
 145 150 155 160
 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
 165 170 175
 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
 180 185 190
 Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
 195 200 205
 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser
 210 215 220
 Met Ser Gly Arg Leu
 225

<210> 66
 <211> 924
 <212> DNA
 <213> Neisseria gonorrhoeae

<220>

09630433.081604

$\langle 222 \rangle \quad (1) \dots (921)$

atg caa tac agc aca ctg gca gga caa acc gac aac tcc ctc gtt tcc 48
Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser
1 5 10 15

aat aat ttc ggg ttt ttg cgc ctg ccg ctt aat ttt atg ccg tat gaa 96
Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
20 25 30

agc cat gcc gat tgg gtt att acc ggc gtg cct tat gat atg gcg gtt 144
Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
 35 40 45

tca ggg cgt tcc ggc ggg cgt ttc ggt cct gaa gcc atc cgg cgc gcc 192
Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
50 55 60

tcc gtc aac ctc gct tgg gag cac cgc agg ttt ccg tgg aca ttt gat 240
 Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
 65 70 75 80

gtg cgc gaa cgc ctg aac att att gat tgc ggc gac ttg gtt ttt tct 288
Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
85 90 95

ttt ggc gac agc agg gat ttc gtc gaa aaa atg gaa gcg cac gcc ggc 336
Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
100 105 110

aaa tta ctt tct ttc ggc aaa cgc tgt ttg agt ttg ggc ggc gac cat 384
Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
115 120 125

ttc att acc ctc cgc ttg ttg cgc gcc cac gcc cgc tat ttc gcc aaa 432
Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
130 135 140

ctc gca ctg att cat ttt gac ggg cac acc gac acc tac gac aac ggc 480
Leu Ala Leu Ile His phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
145 150 155 160

agc gaa tac gac cac ggc acg atg ttt tat acc gcc ccc aag gaa ggc 528
 Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
 165 170 175

ctc atc gac cgc tcc cgt tcc gta caa atc ggc ata cgc acc gaa cac 576
Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
180 185 190

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agt aaa aaa ttg cct ttt act gtg ttg tcc gcc ccc aaa gtc aat gaa 624
Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu
    195                                200                                205

gac agt gtt gaa gag acc gtc cgt aaa atc aaa gaa acc gtc ggc aat 672
Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
    210                                215                                220

atg ccc gtt tac ctg act ttc gac ata gac tgt ctc gac ccg tcg ttc 720
Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
    225                                230                                235                                240

gcc ccc ggg acc ggt acg ccc gta tgc ggc ggc ctg agc agc gac agg 768
Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
    245                                250                                255

gca tta aaa atc cta cgt ggg ctg acg gat ctc gac atc gtc ggt atg 816
Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
    260                                265                                270

gat gtt gta gaa gtt gcc ccc tct tac gac caa tcc gac att acc gct 864
Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
    275                                280                                285

ttg gcc ggc gcc aca att gcc ttg gaa atg ctt tac ctt caa ggt gcg 912
Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala
    290                                295                                300

aaa aaq gac tga
Lys Lys Asp
305

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<210> 67
 <211> 307
 <212> PRT
 <213> Neisseria gonorrhoeae

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<400> 67
Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser
  1                                5                                10                                15

Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
    20                                25                                30

Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
    35                                40                                45

Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
    50                                55                                60

Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
    65                                70                                75                                80

Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
    85                                90                                95

Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
    100                                105                                110

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109180"EEH0E360

Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
 115 120 125

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
 130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
 145 150 155 160

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
 165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
 180 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu
 195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
 210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
 225 230 235 240

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
 245 250 255

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
 260 265 270

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
 275 280 285

Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala
 290 295 300

Lys Lys Asp
 305

<210> 68
 <211> 1404
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1)..(1401)

<400> 68
 atg acd ttg ctc aat cta atg ata atg caa gat tac ggt att tcc gtt 48
 Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
 1 5 10 15

tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tgg gct atg 96
 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30

aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144

0930433 081604

Lys	Ser	Tyr	Phe	Ser	Lys	Tyr	Ile	Leu	Pro	Val	Ser	Leu	Phe	Thr	Leu		
		35					40					45					
cca	cta	tcc	ctt	tcc	cca	tcc	gtt	tcg	gct	ttt	acg	ctg	cct	gaa	gca	192	
Pro	Leu	Ser	Leu	Ser	Pro	Ser	Val	Ser	Ala	Phe	Thr	Leu	Pro	Glu	Ala		
	50					55					60						
tgg	cgg	gcg	gcg	cag	caa	cat	tcg	gct	gat	ttt	caa	gcg	tcc	cat	tac	240	
Trp	Arg	Ala	Ala	Gln	Gln	His	Ser	Ala	Asp	Phe	Gln	Ala	Ser	His	Tyr		
	65				70					75					80		
cag	cgt	gat	gca	gtg	cgc	gca	cgg	caa	caa	caa	gcc	aag	gcc	gca	ttc	288	
Gln	Arg	Asp	Ala	Val	Arg	Ala	Arg	Gln	Gln	Gln	Ala	Lys	Ala	Ala	Phe		
				85					90					95			
ctt	ccc	cat	gta	tcc	gcc	aat	gac	agc	tac	cag	cgc	cag	ccg	cca	tcg	336	
Leu	Pro	His	Val	Ser	Ala	Asn	Ala	Ser	Tyr	Gln	Arg	Gln	Pro	Pro	Ser		
			100					105					110				
att	tct	tcc	acc	cgc	gaa	aca	cag	gga	tgg	agc	gtg	cag	gtg	gga	caa	384	
Ile	Ser	Ser	Thr	Arg	Glu	Thr	Gln	Gly	Trp	Ser	Val	Gln	Val	Gly	Gln		
		115					120					125					
acc	tta	ttt	gac	gct	gcc	aaa	ttt	gca	caa	tac	cgc	caa	agc	agg	ttc	432	
Thr	Leu	Phe	Asp	Ala	Ala	Lys	Phe	Ala	Gln	Tyr	Arg	Gln	Ser	Arg	Phe		
	130					135					140						
gac	acg	cag	gct	gca	gaa	cag	cgt	tcc	gat	gcg	gca	cgc	gaa	gaa	ttg	480	
Asp	Thr	Gln	Ala	Ala	Glu	Gln	Arg	Phe	Asp	Ala	Ala	Arg	Glu	Glu	Leu		
	145				150					155					160		
ctg	tgg	aaa	gtt	gcc	gaa	agt	tat	tcc	aac	gtt	tta	ctc	agc	cga	gac	528	
Leu	Leu	Lys	Val	Ala	Glu	Ser	Tyr	Phe	Asn	Val	Leu	Leu	Ser	Arg	Asp		
				165					170					175			
acc	gtt	gcc	gcc	cat	gcg	gcg	gaa	aaa	gag	gct	tat	gcc	cag	cag	gta	576	
Thr	Val	Ala	Ala	His	Ala	Ala	Glu	Lys	Glu	Ala	Tyr	Ala	Gln	Gln	Val		
			180					185					190				
agg	cag	gcg	cag	gct	tta	ttc	aat	aaa	ggt	gct	gcc	acc	gcg	ctg	gat	624	
Arg	Gln	Ala	Gln	Ala	Leu	Phe	Asn	Lys	Gly	Ala	Ala	Thr	Ala	Leu	Asp		
		195					200					205					
att	cac	gaa	gcc	aaa	gcc	ggt	tac	gac	aat	gcc	ctg	gcc	caa	gaa	acc	672	
Ile	His	Glu	Ala	Lys	Ala	Gly	Tyr	Asp	Asn	Ala	Leu	Ala	Gln	Glu	Ile		
	210					215					220						
gcc	gta	ttg	gct	gag	aaa	caa	acc	tat	gaa	aac	cag	ttg	aac	gac	tac	720	
Ala	Val	Leu	Ala	Glu	Lys	Gln	Thr	Tyr	Glu	Asn	Gln	Leu	Asn	Asp	Tyr		
	225				230					235					240		
acc	gac	ctg	gat	agc	aaa	caa	atc	gag	gcc	ata	gat	acc	gcc	aac	ctg	768	
Thr	Asp	Leu	Asp	Ser	Lys	Gln	Ile	Glu	Ala	Ile	Asp	Thr	Ala	Asn	Leu		
				245					250					255			
ttg	gca	cgc	tat	ctg	ccc	aag	ctg	gaa	cgt	tac	agt	ctg	gat	gaa	tgg	816	
Leu	Ala	Arg	Tyr	Leu	Pro	Lys	Leu	Glu	Arg	Tyr	Ser	Leu	Asp	Glu	Trp		
			260					265						270			
cag	cgc	att	gcc	tta	tcc	aac	aat	cat	gaa	tac	cgg	atg	cag	cag	ctt	864	

00930433-001604

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<210> 69
<211> 467
<212> PRT
<213> Neisseria meningitidis
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<400> 69
Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
1 5 10 15

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30
 Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35 40 45
 Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
 50 55 60
 Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80
 Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
 85 90 95
 Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
 100 105 110
 Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
 115 120 125
 Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
 130 135 140
 Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
 145 150 155 160
 Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
 165 170 175
 Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
 180 185 190
 Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
 195 200 205
 Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
 210 215 220
 Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
 225 230 235 240
 Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
 245 250 255
 Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
 260 265 270
 Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
 275 280 285
 Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
 290 295 300
 Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
 305 310 315 320
 Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
 325 330 335

0903040360

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<211> 696
<212> DNA
<213> Neisseria gonorrhoeae
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<220>
<221> CDS
<222> (1) .. (693)
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<400> 70																
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Met	Lys	Gln	Ser	Ala	Arg	Ile	Lys	Asn	Met	Asp	Gln	Thr	Leu	Lys	Asn	
1				5					10					15		
aca ttg ggc att tgc ggc att tta gcc ttt tgt ttt ggc ggc gcc atc																96
Thr	Leu	Gly	Ile	Cys	Ala	Leu	Leu	Ala	Phe	Cys	Phe	Gly	Ala	Ala	Ile	
			20					25					30			
gca tca ggt tat cac ttg gaa tat gaa tac ggc tac cgt tat tct gcc																144
Ala	Ser	Gly	Tyr	His	Leu	Glu	Tyr	Glu	Tyr	Gly	Tyr	Arg	Tyr	Ser	Ala	
		35					40					45				
gtg ggc gct ttg gct tgg gtc gta ttt tta tta tta ttg gca cgc ggc																192
Val	Gly	Ala	Leu	Ala	Ser	Val	Val	Phe	Leu	Leu	Leu	Leu	Ala	Arg	Gly	
	50					55					60					
ttc cgg cgc gtt tct tca gtt gtt tta ctg att tac gtc ggc aca acc																240
Phe	Pro	Arg	Val	Ser	Ser	Val	Val	Leu	Leu	Ile	Tyr	Val	Gly	Thr	Thr	
65					70				75					80		

gcc cta tat ttg ccg gtc ggc tgg ctg tat ggt gcg cct tct tat cag 288
Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
85 90 95

ata gtc ggt tgc ata ttg gaa agc aat cct gcc gag gcg cgt gaa ttt 336
Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
100 105 110

gtc ggc aat ctt ccc ggg tgc ctt tat ttt gtg cag gca tta ttt ttc 384
Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
115 120 125

att ttt ggc ttg aca gtc tgg aaa tat tgt gta tct gtg ggg gta ttt 432
Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe
130 135 140

gct gac gta aaa aac tat aaa cgt cgc agc aaa ata tgg ctg acc ata 480
Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
145 150 155 160

tta ttg act ttg att ttg tcc tgc gcg gtc atg gag aaa atc gcc ggc 528
Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly
165 170 175

gat aaa gat tgg cga gaa cct gat gcc ggc ctg ttg ttg aat att ttc 576
Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
180 185 190

gac ctg tat tac gac ttg gct ttc cgc gcc ggc aca ata tgc cgc caa 624
Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln
195 200 205

ggc cgc cca cat ttt gga agt agc aaa aaa agc gtc aac atg gca tat 672
Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr
210 215 220

ccg cca act tgc gcc caa gta taa 696
Pro Pro Thr Cys Ala Gln Val
225 230

<210> 71
<211> 231
<212> PRT
<213> Neisseria gonorrhoeae

<400> 71
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1 5 10 15

Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
20 25 30

Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
35 40 45

Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
50 55 60

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr

09030433 081601

65	70	75	80
Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln			
85		90	95
Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe			
100	105		110
Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe			
115	120		125
Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe			
130	135		140
Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile			
145	150	155	160
Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly			
165	170		175
Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe			
180	185		190
Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln			
195	200		205
Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr			
210	215		220
Pro Pro Thr Cys Ala Gln Val			
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 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
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 gaa tac tac gac gcg cgt gcg gcg tgt gag ggc atc aaa ccc gcc tct 96
 Glu Tyr Tyr Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser
 20 25 30
 tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144
 Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
 35 40 45
 aac cgc gcg gac aaa gtc gat ttg cgc acg ctg caa agc tgg ctg ggt 192
 Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
 50 55 60

009180-EEH0360

cag ctg att gag gga aaa cag gaa atc gac ttt cct tgg tat ccg gcg	240
Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala	
65 70 75 80	
cgg gtg gtg tgc cac gat att ctg ggg cag acc gcg ttg gtg gat ttg	288
Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu	
85 90 95	
gca ggt ctg cgc gat gcg att gcc gaa aaa ggc ggc gat cct gcc aaa	336
Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys	
100 105 110	
gtg aat ccg gtg gtg caa acc cag ctc atc gtc gac cac tcg ctg gcg	384
Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala	
115 120 125	
gtg gaa tgc ggc ggc tac gac ccc gat gcg ttc cgc aaa aac cgc gaa	432
Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu	
130 135 140	
atc gaa gac aga cgt aac gaa gac cgt ttc cac ttc atc aac tgg aca	480
Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr	
145 150 155 160	
aaa acc gct ttt gaa aat gtg gac gtg att ccg gcg ggc aac ggc atc	528
Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile	
165 170 175	
atg cac caa atc aat cta gaa aaa atg tcg ccc gtc gtc caa gtc aaa	576
Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys	
180 185 190	
aac ggc gtg gct ttc ccc gat acc tgc gtc ggc acg gat tcg cac acg	624
Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr	
195 200 205	
cca cac gtc gat gcg ctg ggc gtg att tcc gtg ggc gtg ggc gga ttg	672
Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu	
210 215 220	
gaa gcg gaa acc gta atg ctg gga cgc gcg tcc atg atg cgc ctg ccc	720
Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro	
225 230 235 240	
gat att gtc ggc gtt gag ctg aac ggc aaa cgg aag gcg ggc att acg	768
Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr	
245 250 255	
gcg acg gat att gtg ttg gca ctg acc gag ttt ctg cgc aaa gaa cgc	816
Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg	
260 265 270	
gtg gtc ggg gcg ttt gtc gaa ttc ttc ggc gag ggc gcg aga agc ctg	864
Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu	
275 280 285	
tct atc ggc gac cgc gcg acc att tcc aac atg acg ccg gag ttc ggc	912
Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly	
290 295 300	

09030433 084604

att gaa aac gac gta ctc ggc gtt gca gac ggc aaa gaa atc cgc ctg Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu 545 550 555 560	1680
aaa gac att tgg cct acc gat gaa gaa atc gat gcc atc gtt gcc gaa Lys Asp Ile Trp Pro Thr Asp Glu Glu Ile Asp Ala Ile Val Ala Glu 565 570 575	1728
tat gtg aaa ccg cag caa ttt cgc gac gtt tat atc ccg atg ttc gac Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp 580 585 590	1776
acc ggc aca gcg caa aaa gca cca agc ccg ctg tac gac tgg cgt cca Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg Pro 595 600 605	1824
atg tct acc tat atc cgc cgc cca cct tac tgg gaa ggc gca ctg gca Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala 610 615 620	1872
ggg gaa cgc aca tta agc ggt atg cgt ccg ctg gcg att ttg ccc gac Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp 625 630 635 640	1920
aac atc acc acc gac cat ctc tgg cca tcc aat gcg att ttg gca agc Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala Ser 645 650 655	1968
agt gcc gca ggc gaa tat ttg gca aaa atg ggt ttg cct gaa gaa gac Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Asp 660 665 670	2016
ttc aac tct tac gca acc cac cgt ggc gac cac ttg acc gcc caa cgc Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg 675 680 685	2064
gca acc ttc gcc aat ccg aaa ctg ttt aac gaa atg gtg aga aac gaa Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Arg Asn Glu 690 695 700	2112
gac ggc agc gta cgc caa ggt tgg ctg gca cgc gtt gaa ccc gaa ggc Asp Gly Ser Val Arg Gln Gly Ser Leu Ala Arg Val Glu Pro Glu Gly 705 710 715 720	2160
caa acc atg cgc atg tgg gaa gcc atc gaa acc tat atg aac cgc aaa Gln Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys 725 730 735	2208
cag ccg ctc atc atc att gcc ggc gcg gac tac ggt caa ggc tca agc Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser Ser 740 745 750	2256
cgc gac tgg gct gca aaa ggc gta cgc ctc gcc ggc gtg gaa gcg att Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala Ile 755 760 765	2304
gtt gcc gaa ggc ttc gag cgt atc cac cgc acc aac ttg atc ggt atg Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met 770 775 780	2352

09030433 081604

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ggc gtg ttg ccg ctg cag ttc aaa ccg ggt acc aac cgc cac acc ctg 2400
Gly Val Leu Pro Leu Gln Phe Lys Pro Gly Thr Asn Arg His Thr Leu
785              790              795              800

caa ctg gac ggt acg gaa acc tac gac gtt gtc ggc gaa cgc aca ccg 2448
Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro
            805              810              815

cgc tgc gac ctg acc ctt gtg att cac cgt aaa aac ggc gag acc gtc 2496
Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val
            820              825              830

gaa gtc ccc att acc tgc cgc ctc gat acc gca gaa gaa gtg ttg gta 2544
Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val
            835              840              845

tat gaa gcc ggt ggc gta ttg caa cgg ttt gca cag gat ttt ttg gaa 2592
Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu
            850              855              860

ggg aac gcg gct tag 2607
Gly Asn Ala Ala
865

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<210> 73
 <211> 868
 <212> PRT
 <213> Neisseria meningitidis

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<400> 73
Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu
 1              5              10              15

Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser
            20              25              30

Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
            35              40              45

Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
            50              55              60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
            65              70              75              80

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu
            85              90              95

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
            100              105              110

Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala
            115              120              125

Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu
            130              135              140

Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr
            145              150              155              160

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Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile
 165 170 175
 Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys
 180 185 190
 Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr
 195 200 205
 Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu
 210 215 220
 Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro
 225 230 235 240
 Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr
 245 250 255
 Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg
 260 265 270
 Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu
 275 280 285
 Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly
 290 295 300
 Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu
 305 310 315 320
 Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr
 325 330 335
 Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr
 340 345 350
 Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala
 355 360 365
 Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly
 370 375 380
 Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro
 385 390 395 400
 Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser
 405 410 415
 Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala Asn
 420 425 430
 Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro
 435 440 445
 Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro
 450 455 460
 Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr
 465 470 475 480

09830433-084604

Cys	Asn	Gly	Met	Ser	Gly	Ala	Leu	Asp	Pro	Lys	Ile	Gln	Lys	Glu	Ile	485	490	495
Ile	Asp	Arg	Asp	Leu	Tyr	Ala	Thr	Ala	Val	Leu	Ser	Gly	Asn	Arg	Asn	500	505	510
Phe	Asp	Gly	Arg	Ile	His	Pro	Tyr	Ala	Lys	Gln	Ala	Phe	Leu	Ala	Ser	515	520	525
Pro	Pro	Leu	Val	Val	Ala	Tyr	Ala	Leu	Ala	Gly	Ser	Ile	Arg	Phe	Asp	530	535	540
Ile	Glu	Asn	Asp	Val	Leu	Gly	Val	Ala	Asp	Gly	Lys	Glu	Ile	Arg	Leu	545	550	555
Lys	Asp	Ile	Trp	Pro	Thr	Asp	Glu	Glu	Ile	Asp	Ala	Ile	Val	Ala	Glu	565	570	575
Tyr	Val	Lys	Pro	Gln	Gln	Phe	Arg	Asp	Val	Tyr	Ile	Pro	Met	Phe	Asp	580	585	590
Thr	Gly	Thr	Ala	Gln	Lys	Ala	Pro	Ser	Pro	Leu	Tyr	Asp	Trp	Arg	Pro	595	600	605
Met	Ser	Thr	Tyr	Ile	Arg	Arg	Pro	Pro	Tyr	Trp	Glu	Gly	Ala	Leu	Ala	610	615	620
Gly	Glu	Arg	Thr	Leu	Ser	Gly	Met	Arg	Pro	Leu	Ala	Ile	Leu	Pro	Asp	625	630	635
Asn	Ile	Thr	Thr	Asp	His	Leu	Ser	Pro	Ser	Asn	Ala	Ile	Leu	Ala	Ser	645	650	655
Ser	Ala	Ala	Gly	Glu	Tyr	Leu	Ala	Lys	Met	Gly	Leu	Pro	Glu	Glu	Asp	660	665	670
Phe	Asn	Ser	Tyr	Ala	Thr	His	Arg	Gly	Asp	His	Leu	Thr	Ala	Gln	Arg	675	680	685
Ala	Thr	Phe	Ala	Asn	Pro	Lys	Leu	Phe	Asn	Glu	Met	Val	Arg	Asn	Glu	690	695	700
Asp	Gly	Ser	Val	Arg	Gln	Gly	Ser	Leu	Ala	Arg	Val	Glu	Pro	Glu	Gly	705	710	715
Gln	Thr	Met	Arg	Met	Trp	Glu	Ala	Ile	Glu	Thr	Tyr	Met	Asn	Arg	Lys	725	730	735
Gln	Pro	Leu	Ile	Ile	Ile	Ala	Gly	Ala	Asp	Tyr	Gly	Gln	Gly	Ser	Ser	740	745	750
Arg	Asp	Trp	Ala	Ala	Lys	Gly	Val	Arg	Leu	Ala	Gly	Val	Glu	Ala	Ile	755	760	765
Val	Ala	Glu	Gly	Phe	Glu	Arg	Ile	His	Arg	Thr	Asn	Leu	Ile	Gly	Met	770	775	780
Gly	Val	Leu	Pro	Leu	Gln	Phe	Lys	Pro	Gly	Thr	Asn	Arg	His	Thr	Leu	785	790	795

TOPTBO:EE40E350

Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro
805 810 815

Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val
820 825 830

Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val
835 840 845

Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu
850 855 860

Gly Asn Ala Ala
865

<210> 74
<211> 1170
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(1167)

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Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser
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aaa ggc gtg ttt ttc aaa cgt tcc gac ctg ccc gag gcg gcg cgg gaa 96
Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
20 25 30

gcg gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc ccg 144
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
35 40 45

gat ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agc tcg tcc 192
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
50 55 60

acc agc aag gcg gtg att ttg gac aag tcc gaa cgc gcc gat cac gat 240
Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp
65 70 75 80

gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat 288
Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
85 90 95

tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc 336
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110

atc gag caa ggc ttg gtc gat aaa ggc aag att cct tca gac ggc atc 384
Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile
115 120 125

09830433.081601

tgc	aca	gtc	aaa	atc	tgg	cag	aaa	aac	atc	ggc	aaa	acc	att	att	gcc	432
Cys	Thr	Val	Lys	Ile	Trp	Gln	Lys	Asn	Ile	Gly	Lys	Thr	Ile	Ile	Ala	
	130					135					140					
cat	gta	ccg	atg	caa	aac	ggc	gca	gtt	tgg	gaa	aca	ggc	gat	ttt	gag	480
His	Val	Pro	Met	Gln	Asn	Gly	Ala	Val	Leu	Glu	Thr	Gly	Asp	Phe	Glu	
145					150					155					160	
ctc	gac	ggc	gta	acg	ttc	ccg	gca	gcc	gaa	gta	caa	atc	gaa	ttt	ctt	528
Leu	Asp	Gly	Val	Thr	Phe	Pro	Ala	Ala	Glu	Val	Gln	Ile	Glu	Phe	Leu	
				165					170					175		
gat	cca	gcc	gac	ggc	gaa	ggc	agt	atg	ttc	cca	acc	ggc	aat	ttg	gtc	576
Asp	Pro	Ala	Asp	Gly	Glu	Gly	Ser	Met	Phe	Pro	Thr	Gly	Asn	Leu	Val	
			180					185					190			
gat	gaa	att	gat	gtg	ccg	aat	ata	ggc	cgt	ttg	aaa	gcc	acg	ctc	atc	624
Asp	Glu	Ile	Asp	Val	Pro	Asn	Ile	Gly	Arg	Leu	Lys	Ala	Thr	Leu	Ile	
		195					200					205				
aac	gcg	ggc	att	ccg	acc	gtt	ttc	ctg	aat	gcc	gcc	gac	ttg	ggc	tac	672
Asn	Ala	Gly	Ile	Pro	Thr	Val	Phe	Leu	Asn	Ala	Ala	Asp	Leu	Gly	Tyr	
	210					215					220					
acg	ggc	aaa	gag	ttg	caa	gac	gac	atc	aac	aac	gat	gcc	gca	gct	ttg	720
Thr	Gly	Lys	Glu	Leu	Gln	Asp	Asp	Ile	Asn	Asn	Asp	Ala	Ala	Ala	Leu	
225					230					235					240	
gaa	aaa	ttc	gag	aaa	atc	cgc	gct	tac	ggg	gcg	ctg	aaa	atg	ggg	ctg	768
Glu	Lys	Phe	Glu	Lys	Ile	Arg	Ala	Tyr	Gly	Ala	Leu	Lys	Met	Gly	Leu	
				245					250					255		
atc	agc	gac	gta	tcc	gaa	gct	gcc	gcc	cgc	gcg	cac	acg	ccg	aaa	gtc	816
Ile	Ser	Asp	Val	Ser	Glu	Ala	Ala	Ala	Arg	Ala	His	Thr	Pro	Lys	Val	
			260					265					270			
gcc	ttc	gtc	gcg	ccc	gcc	gcc	gat	tac	acc	gcc	tcc	agt	ggc	aaa	acc	864
Ala	Phe	Val	Ala	Pro	Ala	Ala	Asp	Tyr	Thr	Ala	Ser	Ser	Gly	Lys	Thr	
		275					280					285				
gtg	aat	gcc	gcc	gac	atc	gat	ttg	ctg	gta	cgc	gcc	ctg	agc	atg	ggc	912
Val	Asn	Ala	Ala	Asp	Ile	Asp	Leu	Leu	Val	Arg	Ala	Leu	Ser	Met	Gly	
	290					295					300					
aaa	ttg	cac	cac	gcg	atg	atg	ggg	acc	gcc	tct	gtt	gcc	att	gcg	acc	960
Lys	Leu	His	His	Ala	Met	Met	Gly	Thr	Ala	Ser	Val	Ala	Ile	Ala	Thr	
305					310					315					320	
gcc	gcc	gcc	gtg	ccc	ggg	acg	ctg	gtc	aac	ctt	gcc	gca	ggc	ggc	gga	1008
Ala	Ala	Ala	Val	Pro	Gly	Thr	Leu	Val	Asn	Leu	Ala	Ala	Gly	Gly	Gly	
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<210> 75
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 <212> PRT
 <213> Neisseria meningitidis

<400> 75

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			20					25						30	
Ala	Gly	Ser	Ala	Arg	Asp	Lys	Ile	Leu	Leu	Arg	Val	Leu	Gly	Ser	Pro
		35					40					45			
Asp	Pro	Tyr	Gly	Lys	Gln	Ile	Asp	Gly	Leu	Gly	Asn	Ala	Ser	Ser	Ser
	50					55					60				
Thr	Ser	Lys	Ala	Val	Ile	Leu	Asp	Lys	Ser	Glu	Arg	Ala	Asp	His	Asp
	65				70					75				80	
Val	Asp	Tyr	Leu	Phe	Gly	Gln	Val	Ser	Ile	Asp	Lys	Pro	Phe	Val	Asp
				85					90					95	
Trp	Ser	Gly	Asn	Cys	Gly	Asn	Leu	Thr	Ala	Ala	Val	Gly	Ala	Phe	Ala
			100					105					110		
Ile	Glu	Gln	Gly	Leu	Val	Asp	Lys	Gly	Lys	Ile	Pro	Ser	Asp	Gly	Ile
		115					120						125		
Cys	Thr	Val	Lys	Ile	Trp	Gln	Lys	Asn	Ile	Gly	Lys	Thr	Ile	Ile	Ala
		130					135					140			
His	Val	Pro	Met	Gln	Asn	Gly	Ala	Val	Leu	Glu	Thr	Gly	Asp	Phe	Glu
	145				150					155					160
Leu	Asp	Gly	Val	Thr	Phe	Pro	Ala	Ala	Glu	Val	Gln	Ile	Glu	Phe	Leu
				165					170					175	
Asp	Pro	Ala	Asp	Gly	Glu	Gly	Ser	Met	Phe	Pro	Thr	Gly	Asn	Leu	Val
			180					185					190		
Asp	Glu	Ile	Asp	Val	Pro	Asn	Ile	Gly	Arg	Leu	Lys	Ala	Thr	Leu	Ile
		195					200						205		
Asn	Ala	Gly	Ile	Pro	Thr	Val	Phe	Leu	Asn	Ala	Ala	Asp	Leu	Gly	Tyr
	210					215						220			
Thr	Gly	Lys	Glu	Leu	Gln	Asp	Asp	Ile	Asn	Asn	Asp	Ala	Ala	Ala	Leu
	225				230					235					240

09030433 081604

Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu
245 250 255
Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val
260 265 270
Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr
275 280 285
Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly
290 295 300
Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
305 310 315 320
Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly
325 330 335
Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
340 345 350
Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
355 360 365
Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val
370 375 380
Pro Glu Asp Cys Phe
385

<210> 76
<211> 2094
<212> DNA
<213> Neisseria gonorrhoeae

<220>
<221> CDS
<222> (1)..(2091)

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atg aat tcg acc gca agt aaa acc ctg aaa gga ttg tcg ctg gtg ttt 48
Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe
1 5 10 15
ttc gcc tct ggc ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96
Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
20 25 30
ctt cta ttc agc cac ata ggt atc gat ttg agt tcg att act gtc att 144
Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
35 40 45
att tct gta ttt atg gtc ggc ttg ggt gta ggt gcg tat ttc ggc gga 192
Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
50 55 60
cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc 240
Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile

09030433 081604

65	70	75	80	
gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc aag ggt ctg att				288
Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile	85	90	95	
tcc ggc ttg ggg cat ctt tta gtt gag gct gat ttg ccc atc atc gct				336
Ser Gly Leu His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala	100	105	110	
gct gcc aat ttc ctc tta ttg ctg ctt cct acc ttt atg atg ggc gcg				384
Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala	115	120	125	
acc ttg ccc ttg ctg acc tgt ttt ttt aac cgg aaa ata cat aat gtt				432
Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val	130	135	140	
ggc gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt gcg gca				480
Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala	145	150	155	160
ctc gga tgc ctt gcc gcc gcc gaa ttt ttc tac gtc ttt ttt acc ctc				528
Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu	165	170	175	
tcc caa acc att gcg ctg aca gcc tgc ctt aac ctt ctg att gct gct				576
Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Leu Ile Ala Ala	180	185	190	
tca gta tgc tgc gtt aca gaa agg atg gat atg gtg aac act aaa ccg				624
Ser Val Cys Cys Val Thr Glu Arg Met Asp Met Val Asn Thr Lys Pro	195	200	205	
aat act agt gtg att aat atg ctt tct ttc ctt acc gga tta ttg agc				672
Asn Thr Ser Val Ile Asn Met Leu Ser Phe Leu Thr Gly Leu Leu Ser	210	215	220	
ttg ggt ata gaa gtc ttg tgg gta agg atg ttt tgc ttc gca gca cag				720
Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln	225	230	235	240
tcc gtg cct cag gca ttt tca ttt att ctt gcc tgt ttt ctg acc ggt				768
Ser Val Pro Gln Ala Phe Ser Phe Ile Leu Ala Cys Phe Leu Thr Gly	245	250	255	
atc gcc gtc ggc gcg tat ttt ggc aaa cgg att tgc cgc agc cgc ttt				816
Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe	260	265	270	
gtt gat att ccc ttt atc ggg cag tgc ttc ttg tgg gcg ggt att gcc				864
Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala	275	280	285	
gat ttt ttg att ttg ggt gct gcg tgg ttg ttg acg ggt ttt tcc ggt				912
Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly	290	295	300	
ttc gtc cac cac gcc ggt att ttc att acc ctg tct gcc gtc gtc agg				960
Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg				

09030433 001604

305	310	315	320	
ggg ttg att ttc cca ctt gta cac cat gtg ggt acg gat ggc aac aaa				1008
Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys				
325		330	335	
tcc gga cga cag gtt tcc aat gtt tat ttc gcc aac gtt gcc ggc agt				1056
Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser				
340		345	350	
gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttg ttg tcc				1104
Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser				
355		360	365	
acc caa cag att tac ctg ctc atc tgt ttg att tct gct gct gtc cct				1152
Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro				
370		375	380	
ttg ttt tgt aca ctg ttc caa aaa agt ctc cga ctg aat gca gtg tcg				1200
Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser				
385		390	395	400
gta gca gtt tcc cta atg ttc ggc atc ctc atg ttc cta ctg ccg gat				1248
Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp				
405		410	415	
tct gtc ttt caa aat att gct ggc cgt ccg gat agg ttg att gaa aac				1296
Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn				
420		425	430	
aaa cac ggc att gtt gcg gtt tac cat aga gat ggt gat aag gtt gtt				1344
Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val				
435		440	445	
tat ggg gcg aat gta tac gac ggc gca tac aat acc gat ata ttc aat				1392
Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn				
450		455	460	
agt gtc aac ggc atc gaa cgt gcc tat ctg cta ccc tcc ctg aag tcc				1440
Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser				
465		470	475	480
ggc ata cgc cgc att ttc gtc gtt gga ttg agt aca ggt tcg tgg gcg				1488
Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala				
485		490	495	
cgc gtc ttg tct gcc att ccg gaa atg cag tcg atg atc gtt gcg gaa				1536
Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu				
500		505	510	
atc aat ccg gca tac cgt agc ctt atc gcg gac gag ccg caa atc gca				1584
Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala				
515		520	525	
ccg ctt ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt agg				1632
Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg				
530		535	540	
aaa tgg ctg cgt cgc cat cct gat gaa aaa ttc gac ctg att ttg atg				1680
Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met				

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<210> 77
<211> 697
<212> PRT
<213> Neisseria gonorrhoeae
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Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
      20                      25                      30

Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
      35                      40                      45

Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
      50                      55                      60

Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile
      65                      70                      75                      80

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Ala	Glu	Val	Ser	Ile	Gly	Leu	Phe	Gly	Leu	Val	Ser	Lys	Gly	Leu	Ile		
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Ser	Gly	Leu	Gly	His	Leu	Leu	Val	Glu	Ala	Asp	Leu	Pro	Ile	Ile	Ala		
			100					105					110				
Ala	Ala	Asn	Phe	Leu	Leu	Leu	Leu	Leu	Pro	Thr	Phe	Met	Met	Gly	Ala		
		115						120				125					
Thr	Leu	Pro	Leu	Leu	Thr	Cys	Phe	Phe	Asn	Arg	Lys	Ile	His	Asn	Val		
	130					135					140						
Gly	Glu	Ser	Ile	Gly	Thr	Leu	Tyr	Phe	Phe	Asn	Thr	Leu	Gly	Ala	Ala		
145					150					155					160		
Leu	Gly	Ser	Leu	Ala	Ala	Ala	Glu	Phe	Phe	Tyr	Val	Phe	Phe	Thr	Leu		
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Ser	Gln	Thr	Ile	Ala	Leu	Thr	Ala	Cys	Leu	Asn	Leu	Leu	Ile	Ala	Ala		
			180					185					190				
Ser	Val	Cys	Cys	Val	Thr	Glu	Arg	Met	Asp	Met	Val	Asn	Thr	Lys	Pro		
		195					200					205					
Asn	Thr	Ser	Val	Ile	Asn	Met	Leu	Ser	Phe	Leu	Thr	Gly	Leu	Leu	Ser		
	210					215					220						
Leu	Gly	Ile	Glu	Val	Leu	Trp	Val	Arg	Met	Phe	Ser	Phe	Ala	Ala	Gln		
225					230					235					240		
Ser	Val	Pro	Gln	Ala	Phe	Ser	Phe	Ile	Leu	Ala	Cys	Phe	Leu	Thr	Gly		
			245						250					255			
Ile	Ala	Val	Gly	Ala	Tyr	Phe	Gly	Lys	Arg	Ile	Cys	Arg	Ser	Arg	Phe		
			260					265					270				
Val	Asp	Ile	Pro	Phe	Ile	Gly	Gln	Cys	Phe	Leu	Trp	Ala	Gly	Ile	Ala		
	275						280					285					
Asp	Phe	Leu	Ile	Leu	Gly	Ala	Ala	Trp	Leu	Leu	Thr	Gly	Phe	Ser	Gly		
	290					295					300						
Phe	Val	His	His	Ala	Gly	Ile	Phe	Ile	Thr	Leu	Ser	Ala	Val	Val	Arg		
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Gly	Leu	Ile	Phe	Pro	Leu	Val	His	His	Val	Gly	Thr	Asp	Gly	Asn	Lys		
				325					330					335			
Ser	Gly	Arg	Gln	Val	Ser	Asn	Val	Tyr	Phe	Ala	Asn	Val	Ala	Gly	Ser		
			340					345					350				
Ala	Leu	Gly	Pro	Val	Leu	Ile	Gly	Phe	Val	Ile	Leu	Asp	Leu	Leu	Ser		
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Thr	Gln	Gln	Ile	Tyr	Leu	Leu	Ile	Cys	Leu	Ile	Ser	Ala	Ala	Val	Pro		
	370					375					380						
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385					390					395					400		

0983043:081601

Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp
405 410 415

Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn
420 425 430

Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val
435 440 445

Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn
450 455 460

Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser
465 470 475 480

Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala
485 490 495

Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu
500 505 510

Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala
515 520 525

Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg
530 535 540

Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met
545 550 555 560

Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala
565 570 575

Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val
580 585 590

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His
595 600 605

Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala
610 615 620

Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser
625 630 635 640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
645 650 655

Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Arg Met
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093043-061604

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<211> 32

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<210> 82

<211> 35

<212> DNA

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gctctagacc accatgaaaa aatccctttt cgttc 35

<210> 83

<211> 31

<212> DNA

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<220>

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<212> DNA

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<400> 86

gctctagacc accatgaaca cacgcatcat cgtttc 36

<210> 87

<211> 30

<212> DNA

<213> Artificial sequence

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<400> 87

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<210> 88

<211> 34

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<223> Artificial sequence description: PCR primer

<400> 88

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<210> 89
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<400> 91
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<220>
<223> Artificial sequence description: PCR primer

<400> 98
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<210> 99
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<220>

0930433 081604

<400> 99

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<211> 33

<212> DNA

<213> Artificial sequence

<220>

<400> 100

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<212> DNA

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<400> 101

<210> 102

<211> 34

<212> DNA

<213> Artificial sequence

$\langle 220 \rangle$

<400> 102

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<211> 30
<212> DNA
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<220>
<223> Artificial sequence description: PCR primer

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<210> 105
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<400> 107
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<210> 110
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gctctagacc accatgaatg tttacggttt ccc 33

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<210> 112

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<212> DNA

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0903043-03464
T09T50-EE40E860

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<210> 118

<211> 36

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<210> 119

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<400> 120

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gctctagacc accatgccgc aaattaaaat tccc

34

<210> 121

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<223> Artificial sequence description: PCR primer

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29

<210> 122

<211> 33

<212> DNA

<213> Artificial sequence

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33

<210> 123

<211> 29

<212> DNA

<213> Artificial sequence

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<223> Artificial sequence description: PCR primer

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29

<210> 124

<211> 33

<212> DNA

<213> Artificial sequence

0930433-081604

<223> Artificial sequence description: PCR primer

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<223> Artificial sequence description: PCR primer

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cgggatccaa cctgcttcat gggatgattc 29

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<223> Artificial sequence description: PCR primer

<400> 128

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<211> 28

<212> DNA

<213> Artificial sequence

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<223> Artificial sequence description: PCR primer

<400> 129

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